STIC-Biotech/ChemLib

Bunner, Bridget

From: Sent: Thursday, January 23, 2003 2:33 PM

STIC-Biotech/ChemLib To: sequence search Subject:

Hi! I'd like a sequence search performed for case 09/893,348:

85046

1. the amino acid sequence of SEQ ID NO: 19

Thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 305-7148 mailbox 10B19

NE

JUINT OF CONTACT PAUL SCHULWITZ ECHNICAL INFO. SPECIALIST + appendite (703) 305-1954

Searcher:
Phone:
Location:
Date Picked Up: 1/14
Date Completed: 1/14
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic	:.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compagen Etd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71335 standard; peptide; 18 AA
           Schwab ME,
                                                                                                            05-NOV-1999;
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                                                                                                                                                                                                                                                                                           Bovine; neurite growth inhibitor; Nogo; neural cell; myclin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma;
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                                                                                06-NOV-1998; 98US-0107446
                                                                                                                                                                  WO200031235-A2
                                        (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
             Chen MS
                                                                                                              99WO-US26160.
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WPI; 2000 400052/34.
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Nowpo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of

Claim 22; Page 59; 122pp; English.

cranispharyphical specifycas, pinealsma, hiemangichlastema, accustic neuromat, olivadendroglioma, mengaloma, neuroblastema or retinchlastema and dependent tive nerve diseases e.g. Alzheimer's and parkinson's disease. Therapetties which promote Megrativity can be used to treat or provent hyperproblicative or beauty dysproliferative diseases: e.g. psoriaus and tissue hypertraphy. Ricaymes or antisease hypertraphy alterative diseases e.g. psoriaus and tissue hypertraphy. Ricaymes or antisease hypertraphy accides can be used to inhibit production of Nego protein to induce a penetation of neurons or to promote structural plasticity of the CNS in discribers where nourite growth, regeneration or maintenance are deficient or decired. The animal models can be used in disposite and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a bovine papide p472 used for antiserum 472. Al 472) production. This peptide is similar to rat Nego protein for prevent sequence is designated as SEQ ID No. 3 in the opposition and SEQ ID No. 3 in the opposition and SEQ ID No. 3 in the opposition and SEQ ID No. 2 in the opposition of the control of the specification. However, the disclosure of the specification However, the specification of the The patent relates to neurite growth inhibitor Mogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Mogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neopla disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, necplastic

18

Owery Match Best Total AAY71400 standard, Sequence 18; SYPSIKLEPENPPPYEEA 18 Similarity 100 18; Conservative 0%, Gasro 99; DB 21, Longth 1 0%, Fred. Mo. 1.2e-97; O; Mismatches 0; Indels Length 18, . Gaps 0

2 NOV-2500 (first entry)

central nervous system, neuplastic disease, antiproliferative, glioma, antiprose gene therapy, neuroblastoma, menagioma, retinoblastoma, dependentive neuroblastoma, alzheimer's disease, Parkinson's disease, hyperproliferative disease, benign dysproliferative diseaser diagnosis, programming, tissue hypertrophy, neurobal regeneration, treatment, structural planticity, screening, mutant, mutein. Pat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

Pat Node A protein fragment used in the construction of mutant NiG-D20

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> considering the symplems, epochymna, pinelinau, haddustically addustic concerns, oligodendroglioma, menagicma, neuroblastoma or retinoblastoma of energy and degenerative nerve diseases. Alzheimer's and Parkinson's confissases. Therapeutics which promote Regalactivity can be used to treat or greyent hyperproliforative or benign dysproliforative disorders e.g. of psoriasis and tissue hypertrophy. Pibogymes or antisense Mogo nucleic acids can be used to inhibit production of Nogo protein to induce or regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, respectation or maintenance are conficient or desired the animal medels can be used in diagnostic and screening methods for predisposition to disorders and to screening methods for predisposition to disorders and to screen for or test meletules which can treat or fragent is at Mogo at protein sequence is a fragment of that Mogo at protein sequence is a fragment of the Mogo at Aleiton materials were used for mapping the inhibitory sites of Mogo at Sequence from amino acids 172-974, particularly amino acids of the resultant and manno acids 172-974, particularly amino acids of the meaning and to protein materials and region 1.171 was found to be inhibitory and the inhibitory and the inhibitory sites of the constant and the constant and the second of the constant and 542-722. In addition, is commended to NHH 3T3 fibricklast spreading.
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> to NHH 3T3 fibricklast spreading.
>
> Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers are referred in claim 32 and SEQ ID 35. 25 in disclosure of the are referred. However, the specification does not include sequences. The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying nourite growth inhibitory activity are used in the treatment of height tio disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, Example, Fage , 122pp, English. Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneral WPI; 2000-400052/34 Schwab ME, Chen MS (CHEN/) (SCHW/) SCHWAB M E. (CHEN/) CHEN M S. inducing tegeneration

Matches Query Match Cocal 18; h Similarity 100.0%; Fred. No. 1.: 18; Conservative 0; Mismatches PB 21; .30-06; Length 181; Indels 0;

0

Sequence

181 AA;

SEQ ID numbers 35 42

sequences for

RESULT 3 AAY71390

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82 SYDSIKLEPENPPPYEEA 99

SYDSIKLEPENPPPYEEA 18

AAY71390 standard; Protein; 356 AA

02 NOV 2000 (first entry)

Rat Mogo A protein fragment used in the construction of mutant NiO

central nervous system; neoplastic disease; antiproliferative; glioma; antipense gene therapy; neuroblastoma; dengatoma; retinoblastoma; degenerative networks disease; Alzheimer; parkinson's disease; kyperproliferative disorder; benign dysproliferative disorder, diagnosic; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein. Rat; neurite growth inhibitor, Nogo A, neural cell, myclin; CNS;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benigh dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The present sequence is not given in the specification but is derived from rat 1050 A sequence shown in AAY/1310. SEQ ID number: N5-42 are referred in claim 32 and SEQ ID No: 29 in disclosure of the specification. However, the specification does not include sequences for
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contractions, the gradient, gliceman, delibertanisma, increasing the construction of meuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alibeimer's and parkinson's construction which promote Norman entirity can be used to treat or prevent hyperproliferative or benigh dysproliferative disorders e.g. acids can be used to inhibit production of mysproliferative disorders e.g. constructive disorders e.g. construction of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are constructed methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogarian taging the tradyfortes of Nogo-A sequence as 172-189 + 619-974/His-tag.

CC Nogo A delection mutants were used for mapping the inhibitory sites of Nogo A recent from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to Note: The present sequence is not given in the specification but is composed of the gradient sequence is not given in the specification but is green referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these sequences for the specification of the specification does not include sequences for the specification does not include sequences for these sequences for the specification does not include sequences for these sequences for the specification does not include sequences for the specifica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin matterial with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glicma, glicblasroma, mediallohlastoma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHEN/) CHEN M S
                        specification. However, the these SEQ ID numbers.
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brunopharyngioma, epuddysma, pinealoma, haemangloblascoma, acoustic pourroma. Alignomic plices, megagioma, neurophascoma or retinoblascoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Mogo activity can be used to treat or prevent hypercaliferative diseases. Therapeutics which promote Mogo activity diseases was general and thisme bypertrophy. Therapeutics or notisease Mogo nucleic acids can be used to inhibit production of Mogo protein to induce requestation of massed to inhibit production of Mogo protein to induce requestation of which is grown, regeneration or maintenance are deficient or desired. The animal models can be used in dispositic and screening methods for predisposition to disorders and to screen for or test moderules which can treat or prevent disorders or diseases of the INS. The present separation is a fragment of rat Mogo A protein shown in AMY71317, which is used in the construction of mutant MiG-D4. MiG-D4. Big taying a series of the individual of MiG-D4. MiG-D4. Mig D4. Alchert which can used to the construction of mutant MiG-D4. MiG-D4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nutively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic discuss of the CNS e.g. glioma, glioblastoma, medulloblastoma,
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       A deletion
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mutants were used for mapping the inhibitory
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130.0%, Fred. No. 2 96-96;
^ Mismatches 9, Indols
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Mote. The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-43 are referred in claim 35 and SEC ID MG 79 in disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; neurite growth inhibitor, Mogo A, neural cell, myclin, CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzeelmer's disease, Parkinson's discase; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
                                                        Example, Page -, 122pp; English.
                                                                                                    Nego proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regenerat
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                                                                                                                                                                                                                                                                                                                                                                                  sequence shown in AAY71310"
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Pred. No. 3.7e-06;
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The patent relates to neurite growth inhibitor Mogo which is free all central nervous system (CMS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurit

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   Schwab ME,
                                                                                                                                                             06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     central nervous system, neuplastic disease; antiproliferative; gliona; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
                                                                 (CHEN/) CHEN M S.
                                                                                                                                                                                                                           1666I.AOM-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Par Nage A protein fragment used in the construction of mutant NiG-D3.
                                                                                                                                                                                                                                                                                                                                                          W0200031235 A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71388 standard; Protein; 552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY71388;
                                                                                            (SCHW/) SCHWAB M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 SYDSIKLEPENPPPYEEA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tĥese SEQ ID numbers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth inhibitory activity are used in the treatment of neoplastic disease of the CMS e.g. glioma, glioblastoma, medulloblastoma,
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                                                                                                                                                             98US-0107446
                                                                                                                                                                                                                    99W0-US16160.
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د
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PD PN XXX
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CC Note: The present sequence is not given in the specification but is certification. However, the specification does not include sequences for these SEO ID numbers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                      antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degeneralive nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psormasis; tissue hypertrophy; neuronal regeneration; treatment;
                                                                                                                                                                                                           Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma;
                                                                              Rattus sp.
                                                                                                           structural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                         Rat Nogo A protein fragment used in the construction of mutart Nig-D10
                                                                                                                                                                                                                                                                                                                             02-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        AAY71394 standard; Protein; 684 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulliblastoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 SYDSIKLEPENPPPYEEA 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders of the central nervous system and inducing regeneration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nogo proteins and nucleic acids useful for treating neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-400052/34.
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100.0%;
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Pred. No. 4.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 552;
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W0200031235-A2

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The control of reveals that the problem into the tree of the control of the reveals system (NS) myells material with which it is noticed by the reveals system (NS) myells material with which it is now that the control of the reaction of t
Ext; security nowth inhibitor; Nogo A; neural cell; myelin; CN central pervecus system; neeplactic disease; antiproliferative; introduce deno therapy, neurobiantoma; menagioma; retinoblasto
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                                                                                                                                                                                                           PHT Note A protein fragment used in the construction of mutant NiG D2
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                                                                                                                                                                                                                                                                                                               T. W.A. T. S.
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                                                         glioma
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AAY71399 ID AAY7

AAY71399 standard, Frotein, 732 AA

RESULT 10

450

1 SYDSIKLEPENPPPYEEA 18 SYDSIKLEPENPPPYEEA 469

Matches Query Match

Local

Similarity

100.08; Score 99; DB 21; 100.08; Pred. No. 5.6e-06; tive 0; Mismarches 0;

Length 695;

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On deficient or desired. The adimal models can be used in displace to and reservating methods for predisposition to disouders and to screen for an feet models which can treat prevent disouders and to screen for a feet model, which is can treat treat prevent disouders or displaced of the pascent selection of all Model A protein blood in AAYTING, which is used in the construction of matant MGCD2. Not 20 for is our presed of His-tag/MT-tag/MB A sequence as 172 800/His tag. On MogelA delegion materials were used for mapping the inhibitory stock of the MogelA delegion materials were used for mapping the inhibitory stock of the MogelA delegion for an addition. According to the behavior of the protein Major inhibitory region was identified in the condition of 42-722. In addition, N-terminal region in 171 was found to be inhibitory to NIH 373 fibroblast spreading.

CO Note: The protein sequence is not given in the specification but is determined the class of the second of the specification. History, the specification less not include dequences for these SEO ID numbers.
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Sequence
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                                                                   specification. However these SEQ ID numbers.
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disorders of the central nervous system and inducing regeneration
neurons -
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695 AA;
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craniopharyngioma, ependyoma, pinealoma, medulioblastoma, acoustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. posoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in dispostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant NiG-D18 is composed of His-tag/TT tag/Mgg A sequence from aming acids 172-974, particularly aming acids in the Nogo A sequence from aming acids 172-974, particularly aming to his inhibitory in the present sequence is not given in the specification but is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The parent relates to neutrite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin matterial with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nogo A protein fragment used in the construction of mutant NiG D18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Corresponds to residues 261-974 of Nogo
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        The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (2NS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS = globa, glicha, glichlastona, medalloblastona, cranicpharyogiona, grendyoma, plinaliona, hadraelgi-blystona, cristic neurona, oligodendrogliona, menagiona, neuroblastona or retiroblastoma
                                                                                                                                                                                      Mogo proteins and nucleic acids useful for treating neeplastic disorders of the central nervous system and inducing regeneration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  central nervous system, necplastic disease, antiproliferative, glioma; antisense gene therapy neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease, Alzheimer's disease, Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis, tissue hypertrophy, neuronal regeneration; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for specification.
                                                                                                                                       Example; Page -; 122pp; English.
                                                                                                                                                                                                                                                                    Schwab ME,
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 99WO-US26160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note: "Corresponds to residues 257-274 of Mogo sequence shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note: "Corresponds to residues ITC 189 of Mojo A sequence shown in AAY71310" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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degenerative nerve diseases e.g. Alzheimer's and

Parkinson's

his cases. The appearance which promote Nogo activity can be used to treat or prevent hyperpolificative or benigh dysproliferative disorders e.g. programme and cannot be inhibit production of Nogo protein to industriate and be unded to inhibit production of Nogo protein to industriate and of neurons of the product extraction or maintenance are deficient of the white months production to also be used in dispositive and surround the which can intent to dispositive to dispositive and industrial planticity of the THO 1997. The production to dispositive to dispositive and the specific and surround to produce the production of the surround production of the surround for the dispositive of dispositive and industrial to dispositive and the surround to prevent dispositive and inspects of the THO 197. NIG 197 is composed of the surface of the industrial to the surface of th

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Fat Memo A protein fragment used in the construction of mutant NiG-D1.

Fit; neutite spreach inhibitor; Nogo A; neural cell; myelin; CNS; could be nowned spreach; neighbor; disease, pripreliferative; glioma, introduce the open through; neutablatical, merupicma, refineblastical, dependentive nerve disease; Alzheimer's disease; Parkinson's disease; byesti liferative troduce; life, John M. Myelliferative listiae, lidjest percontess; tissue bypertrophy, help Myelliferative listiae, lidjest produced bypertrophy, neuronal regeneration, treatment; structural plasticity, surreging mutant; mutelin. glioma,

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Region

/note= "Corresponds to residues sequence shown in AAY71310"

/note "Corresponds to residues 172-134

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Location/Qualifiers

Region

Rattus sp.

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Nery proteins and has been acids usoful for treating meaplastic treat elsewhere the register and inducing regeneration

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disease of the CNS e g given, product and mediciplication, decided and degenerate and degenerative nerve diseases e g. Alpharent and new diseases. Therapeutics which promote Nego activity can be used to treat to generative nerve diseases. Therapeutics which promote Nego activity can be used to treat to pseriasis and degenerative nerve diseases. The promote Nego activity can be used to treat to pseriasis and this to be prevent by the promote Nego activity can be used to treat to pseriasis and tissue by extrictly. Sit zyme in All Scales in the induce of regeneration of neutrino growth, regeneration or maintenance are to indiscrete where neutring growth, regeneration or maintenance are to test malecules for predisposition and diseases of the screening methods for predisposition of Asympton and the screening repredisposition of the Nego and the screening repredisposition of the Nego and the screening repredisposition of the Nego and the screening repredisposition of mapping the inhibitory sites of the corporate search of the meant and the corporate search of the Nego a deletion mentals were used for mapping the inhibitory sites of the protein. Major inhibitory region was identified in the cold of the protein sequence is used for mapping the inhibitory animo acids to Nego a deletion of mentals spreading.

The Asympton is sequenced to the protein and the spreading of the inhibitory animo acids of the protein as sequenced in the special fibroblast spreading.
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                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                          these SEQ ID numbers.
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100.0%; Score 99; DB 21; 100.0%; Fred. Mo. 5.9e 06;
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             SYDSIKLEPENPPPYEEA 18
SYDSIKLEPENPPPYEEA 469
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Pat; neurite gr.wth inhibitor, Nojock, neural cell, myclin, CNS; central nervous system; neoplastic disease; antiproliferative; glroma; antisense gene therapy; neuroblastema; menagicma; retinoblastoma; degenerative nerve disease; Alzheimer; disease; Parkinson's disease; byperproliferative disease; Pathology; houronal regeneration treatment; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Nogo A protein fragment used in the construction of mutant Nio-D7
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W0200031235-A2

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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Mcgo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, or retinoblastoma and degenerative nerve diseases. glioblastoma, neuroblastoma are retinoblastoma and degenerative nerve diseases e.g. Alphaimer's and parkinson's diseases. Therapartics which promote Nogo activity can be used to treat regeneration of neurons or to promote Nogo activity and parkinson's acids can be used to inhibit production of Nogo protein to indice regeneration of neurons or to promote structural plasticity of the CNS in discreters where neurity growth, respend tion or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for pre-disposition or discreters and to screen for or test molecules which can treat or prevent discreters and to screen for or test molecules which can treat or prevent discreters and to screen for or test molecules which can treat or prevent discreters or diseases of the CNS. The prosent sorpunce is derived by fusing two fragments of rat Nego A protein shown in AAV71310, which is used in the construction of mutant Nector and the screening two fragments of rat Nego A protein shown in AAV71310, which is used in the construction of mutant Nector and the screening two fragments of the Nego Protein Major inhibitory region was identified in the Nego Protein major inhibitory region was identified in the Nego Protein service of the State of Nego Protein major inhibitory region be inhibitory amine acids to NH in its desired to the inhibitory service is not deep the inhibitory that is not negotially and the inhibitory that is not negotially and the inhibitory service is not deep the inhibitory that is not negotially and the inhibitory that is not negotially and the inhibitory service.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noge protries and nucleic arids useful for treating mesphastic disorders of the central nervous system and inducing regeneration of
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these SEQ ID numbers.
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02-NOV-2000 (first entry)
                                                                                          AAY71562;
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100 0%; Pred No Ke-OK;
Tive 0; Mismatches 0; Indels
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Fat Nego A protein fragment used in the construction of mutant NiG

Вb

452 SYDSIKLEPENPPPYEEA 469

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                                                                                                                                                                                        CC or prevent typerproliferative or tening dysproliferative disorders e.g. CC gentiasis and tissue hypertriply. Filenymes it antisense Mig-nucleic CC acids can be used to inhibit production of bego protein to induce regeneration of neutrons or to promote structural playshmity of the MS of in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in disquestic and screening methods for predisposition to disorders and to screen for or cest molecules which can theat of prevent disorders in disquestic and CC CMD. The present sequence is a fragment of rat Dogo A protein shown in CC CMD. The present sequence is a fragment of rat Dogo A protein shown in CC CMD, which is used in the construction of mytant Mig. The mutant is composed of his-tag/T7-tag/Nogo-A sequence as 172-974/His-tag.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of CC Nogo A sequence from acids 172-974, particularly amino acids CC Nogo A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence from amino acids 172-974, particularly amino acids CC NOGO A sequence acids 172-974, particularly amino acids CC NOGO A sequence acids 172-974, particularly amino acids CC NOGO A sequence acids 172-974, particularly amino acids 172-974.
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                                                                                                                                                                                                                                                                        Note. The present sequence is not given in the specification but is derived from rat Nego A sequence shown in AAY71310 SEQ ID numbers 35.42 are referred in claim 21 and SEQ ID No. 20 in disclosure of the specification. However, the specification does not include sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, accustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and parkinson's diseases. Therapeutics which prompte Negriarivity can be used to treat diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth inhibitory activity are used in the treatment of neople
disease of the CNS e.g. glioma, glioklastoma, medulloblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mago proteins and nucleis worlds useful for treating neighborian of disorders of the central nervous system and indusing regeneration of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
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                                                                                                                                                                                                                                                  these SEQ ID numbers.
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                                                            100.0%; Score 99; DR 21; 100.0%; Pred No. 6 se-06; Mismatches 0;
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AAV71160 grammard; Protein; 974 AA.

WA771545)

or Mov 2000 (first entry)

Fut Nogo A protein fragment used in the construction of mutant NiAext.

Fit, notite powth inhibitor, Noyo A, noural cell, myelin, CNS, control corrects system; complete in disease; antiproliferative; glicma; intiscuse gene therapy; neuroblastoma; menagioma; retinoblastoma; herderen ine neuro disease; Alzheimer's disease; Parkinson's disease; kyperproliferative its adver; benden deporaliferative disease; diagnosis; georiasis; tisume hypertrophy; neuronal regeneration; treatment; structural plasticity; sorrening; mutant; mutein.

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Schwid ME, Chen MS;

PI, 2000 400052/44

Note the define and mathematical useful for treating medplastic disorders of the central nervous system and inducing regeneration of secures:

Example: Page ; 122pp; English.

The putral relates to neurite growth inhibitor Nogo which is free of ill control network system 2008) myelin material with which it is not rely issociated. Note proteins and fragments displaying neurite from the treatment of neeplastic displaying in the VS -4. qlioma, qloblastoma, meduliphiastoma, meduliphiastoma, acoustic neurons, oliophendroglioma, menagioma, haemangioblastoma, acoustic neurons, oliophendroglioma, menagioma, haemangioblastoma, acoustic neurons, oliophendroglioma, menagioma, haemangioblastoma, acoustic neurons of the object of the properties of the promote structural parkinson's his essentialist and tissue bypectific production of Nogo activity can be used to treat a precedent of neurons or to promote Nogo protein to induce responsible and tissue bypectific production of Nogo protein to induce of colors and to instance are deficient or desired. The animal models can be used in diagnostic and research which can read to prevent disorders and to screen for or the construct methods for prevent disorders or diseases of the NS. The prevent is appreciate in the construction of mutant NiAext. The mutant is expected in the construction of mutant NiAext. The mutant is expected in the construction of mutant NiAext. The mutant is expected in the construction of mutant NiAext. The mutant is expected in the inhibitory sites of the No A deletion mutants were used for mapping the inhibitory sites of the No A deletion mutants were used for mapping the inhibitory sites of the No A deletion of mutant series and region 1-171 was found to be inhibitory which the inhibitory along the inhibitory along the inhibitory along the inhibitory and seguence is not given in the specification but is between the inhibitory and seguence of the neutron of the protein in the specification but is between the inhibitory and seguence for the protein in the specification but is not protein in the specification but is not protein in the specification but is not protein the inhibitory and seguence for the mutants and seguence for the m

three SEC ID numbers.

SQ Sequence 974 AA;

Query Match

100.0%; Score 99; DB 21; Length 974;
Best Local Similarity 100.0%; Prod. No. 8e-06;
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1 SYDSIKLEPENPPYEEA 18

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Search completed: January 24, 2003, 11:10:33 Job time - 36 secs

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A;Molecule type: DNA
A;Residues: 1-2957 <DAV>
A;Residues: 1-2957 <DAV>
A;Cross-references: EMBL:AF067617; PIDN:AAC17550 [; GSPDR:GM00019; CESP:T04D1.4

A;Introns: 122/3; 293/3; 515/3; 1205/2, 1577/1; 2221/3, 2776/1, 2864/3

A; Map position: A; Gene: CESP: T04D1.4

Matches Query Match Best

Local Similarity hes 7; Conserv

Conservative

51.5%; Score 51; DB 53.8%; Pred. No. 67; tive 4; Mismatches

DB 2; Length 2957;

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C; Genetics:

A; Experimental source: strain Bristol N2; clone T04D1

A;Status: preliminary; translated from GB/EMBL/DDBJ

No.

gans 0 #text_change 20 Oct 1999 TO4D1.	RESULT 1 T33152 T33152 T33152 C;Species: Caenorhabditis elegans C;Dare: 29-Cort-1999 #sequence_revision 29-Cort-1999 C;Accession: T33152 R;Davidson, S.; Wohldmann, P. submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cosmid T0 A;Reference number: Z21292 A;Accession: T33152	; C gan re bra	TO4D1.4 dditis ele #sequence dmann, P. IL Data Li eequence cequence Z21292	otein T orhabdi 152 1152 Wohldm Wohldm bhe sequencer: 20	ical prosserving ical prosserving in a prosecution in the prior in the prior runhing in a runhing in	RESULT 1 T33152 hypotein T04D1 C.Species: Caenorhabditis C.Date: 29-Cut.1999 #seque C.Accession: T33152 R.Davidson, S.; Wohldmann, submitted to the EMBL Data A,Description: The sequenc A;Peference number: Z21292 A,Accession: T33152
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rotein - avi	VFIHB1	Н	3951	44.4	44	44
DNA topoisomerase	S44861	۲3	2434	44.4	44	43
female sterile hom	A56619	N	754	44.4	44	42
hypothetical prote	T15073	64	661	44.4	44	41
interferon-regulat	A31203	2	631	44.4	44	40
hypothetical prote	T00853	Ŋ	613	44.4	44	39
protein T12A7.2 [i	G88846	t٥	520	44.4	44	8 8
hypothetical prote	T24856	• >	£A;	44.4	ئ و مئو	37
nitrate transport	S77389	2	446	44.4	44	36
interferon regulat	A30819	ę,	423	44.4	44	35
hypothetical prote	T00463	د ا	413	44.4	44	34
ubiquitin-protein	S36769	N	250	44.4	44	33
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peroxisome prolife	JC5777	73	505	45.5	45	30

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A;Molecule type: DNA
A;Residues: 1-442 <MER>
A;Residues: 1-442 <MER>
A;Residues: 1-452 references: EMEL-C19598; NID g1154896; FIRM CAA73656 1; FIRM E218077; PID:g1181934
A;Cross-references: EMEL-C19598; NID g1154896; FIRM CAA73656 1; FIRM E218077; PID:g1181934
B;Merchan, E; Prieto, R.; Kindle, K.L.; Llama, M.J.; Serra, J.L.; Fernandez, E.
Plant Mol. Biol. 27, 1037-1042, 1995
B;Title: Isolation, sequence and expression in Escherichia coli of the nitrite reductase
A;Reference number: S56640; MUID:95284340; PMID:7766873 R;Merchan, F.; Kindie, K.L., Llama, M.J.; Sorra, J.L.; Fornandez, E. Flant Mol. Biol. 28, 759-766, 1995
A;Title: Cloning and sequencing of the nitrate transport system from the thermophilic, fi cus sp. PCC 7942.
A;Reference number: S58738; MUID:95375238; PMID:7647306 A;Accession: S56641 A;Status: nucleic acid sequence not shown; translation not shown nitrate-binding protein nrtA precursor, periplasmic [similarity] - Phormidium C,Species: Phormidium laminosum C,Species: 10-Apr:1996 #sequence revision 19-Apr:1996 #text_change 20-Oct-2000 C,Accession: S58738; S56641; S62124 A; Accession: S58738

A; Molecule type: DNA

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rarbonate transport bitarbose binding probels ompA (imported) - Moster sp. (strain Reperture Notes of sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 Acression: Appl65
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Biol. Chem. 270, 8487-8494, 1995
Title- The major protein of quayale rubbet patticles is a cytochrome P450. Characteria
Paference number: A56377; MUID:95238331; PMID:7721745
Accession: A56377
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Experimental source: strain PCC 7120
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Tross-references: EMBL-219698
Pote: The nucleotide organize was submitted to the EMBL Data Library, Tabuary 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YDSIKLEPENPPPYEEA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.22
                                                                                                                                                                                                                                                                                                                                                                       Watch 49.5%, Score 49, DR 2; Length 458; coal Similarity 50.6%, Fred. No. 16, Indels 7; Compervative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSULATED AND ACCOUNTS IN THE SECOND ASSURED THE SECOND ASSURED TO SECOND ASSURED THE SEC
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Similarity 47.1%; Earry 50, DP 0,
Similarity 47.1%; Exed, No. 11;
B, Conservative %; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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47.1%, Fred. No. 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dength 440
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                                  A;Accession: T43249
A;Status: preliminary; translated from GB/EMBL/DDHJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene
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R;Housen, I.; Demonte, D.; Lafontaine, D.; Vandenhaute, J. submitted to the EMBL Pata Library, December 1995
A;Description: Cloning and comparative analysis of the SpRIM:
A;Reference number: Z22366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dimethylase - fission yeart (Schizosaccharomyces pombe)
(;Species: Schizosaccharomyces pombe
;;Date: 03-Dec-1393 #sequence_revision 03-Dec-1333 #text_change 21-Jan-2000
C,Accession: T40240
F,Portym, F, Back, A.; Painhardt, P, M.D.-3311, F.C., Pajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
Submitted to the EMBL Data Library, October 1999
                                                                                                             C;Species: Schliosaccharomydes pombe
C;Date: 11.Jan.2000 #sequence_tevision 11 Can.2000 #text_change 11-Jan.
C;Accession: T41249
R;Housen, I.; Demonte, D.; Lafontaine, D.; Vandenhaute, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position, 2
A;Introns: 45/3
C;Superfamily: rRNA (adenine-N6-)-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source, strain 972h-; cosmid c336 c. Genetics.
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A;Thtrons 13/2, 132/2, 220/3; 216/2; 307/1; 401/2, 508/3; 734/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C24G7.5 - Caenorhabditis elegans . Stephes. Gaenorhabditis elegans . Stephes. Gaenorhabditis elegans . Cybate 15-Oct-1999 #seguence_revision 15-Oct-1999 #tevt_change 15-Oct-1999 Cybate 15-Oct-1998 #seguence_revision 15-Oct-1999 #tevt_change 15-Oct-1999
                                                                                                                                                                                                                                                                N;Alternate names: dimethylase
                                                                                                                                                                                                                                                                                              rENA (adenine-M6, M6.) -dimethyltransferase (EC 2.1.1.) - fission yeart .orbitrastoonyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-307 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: 221916
A;Accession: T40240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1398 <GOE>
A;Cross-references. EMPL "RM-10; PIEM-AAR42330-1; Carres.Ghebels; CESE:C24G7.
A;Experimental source: strain Bristol N2; clone C24G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, February 1997
A,Festription. The sequence of C. elegans cosmid
A,Reference number: 200352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Goela, D.; Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross references: EMBL:AL121815, FIDR:CAR58154.1, GSFDR:GNecoes, GFDB:CFSC (96.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary, translated from GB/EMBL/DBBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.5%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 YDYLRIQPKKPPPTVE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 VRIEPKNPPPPLAFEE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IKLEPENPPP---YEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YESIKLEPENPPPYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPDB-SPRCIRE 02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 2; Length 1398; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.5;
Fred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 307;
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tches
                                                                             ery Match
                                                                                                                         perfamily: Pyrococous abyssi hypothetical protein PAB1661
                                                                                                                                                           ne: PAB1661
                                                                                                                                                                                            xperimental source: strain Orsay
                                                                                                                                                                                                  ross-references: GB:AJ244786; GB:AL096836; NID:g5458366; PIDN:CAB49979.1; PID:g545849
                                                                                                                                                                                                                                     plecule type: DNA
esidues: 1-257 <KAW>
                                                                                                                                                                                                                                       nonymous, Genoscope
mitted to the EMBL Data Library, July 1999
sscription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
sterence number: A75001
scession: F75084
                                                                                                                                                                                                                                                                                                                                                                                                 ccession: F75084
                                                                                                                                                                                                                                                                                                                                                                                                     pecies: Pyrococcus abyssi
ate: 20-Aug-1999 #seguence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 othetical protein PAB1661 - Pyrococcus abyssi (strain Orsay)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uperfamily: arenavirus zinc finger protein eywords: PNA binding; zinc finger 2-54/Region. zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ap position: segment L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ross-references. GB:M27633; MID:g33l385; PIDN:AAA46268.1; PID:g33l386
Omment: This protein may act as an RNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      olecule type: genomic RNA
esidues: 1-90 <SAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walvato, M.S.; Shimomaye, E.M.
rology 173, 1-10, 1989
ritle: The completed sequence of lymphocytic choriomeningitis virus reveals a unique R
reference number. A32535, NGID: 90051057; PMID: 2510401
recession: A32592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nc finger protein - lymphocytic choriomeningitis virus (strain Armstrong 53b)
pecties: lymphocytic choriomeningitis virus
pate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pescription: dimethylation of two adjacent adenosines from the 3' end of the 18SrRNA Superfamily: rRNA (adenine-N6-)-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Function:
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                                                                                                                                                                               netics
                                                      Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 ISTAPSSPPPYEE 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 VRIEPKNPPPPLAFEE 216
            2 YDSIKLEPEMPEP 14
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                                                      Conservative
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                                                                       50.0%;
                                                 3; Mismatches
                                                                     Score 47; DB
Fred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.5; |
Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                      DB 2; Length 257;
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                                                 2; Indels
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                                             0;
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                                           Gaps
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A; Molecule type: mRNA
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Peroxisome proliferator activated receptor gamma 2 - human (fragment)
N;Alternate names: peroxisome proferator activated receptor gamma 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C;Accession: PC4290
R;Yanase, T; Yashiro, T; Takitani, K; Kato, S; Taniguchi, S; Takayunagi, R; Nawata, Biochem. Biochys. Pes. Commun. 233, 329-324, 1997
A;Title: Differential expression of PPAP gamma 1 and gamma 2 isoforms in human adipose ti
A;Reference number: PC4290; MUID:97289627, PMID:9144532
A;Accession: PC4290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 384, 276-279, 1996
A;Title: 20S cyclosome complex formation and proteolytic activity inhibited by the cAMP/LA;Reference number: Z25896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: stil+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein stil+ - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct_2000 #sequence_revision 20 Oct_2000 #fext_change 20-Oct_2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-591 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Yamashita, Y.; Nakaseko, Y.; Samejima, T.; Kumada, K., Yamada, H., Yanagida, M.
Nature 384, 276-279, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:D85197; PIDN:BAA22619.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL049498; PIDN:CABR9910 1; GSPDB:GN00068; SPDB:SPCC645.14c A;Experimental source: strain 972h-; cosmid c645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, March 1999
A;Peference number: Z22000
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C;Date: 03-Dec-1999 #sequence_revision 03 D=c-1999 #:0x*
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Local Similarity 55.6%;
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Molecule type: DNA
Pesidues: 1-156 <8TO>
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Date: 10-May 2001 #sequence revision 10 May-2001 #text_change 10-May-2001
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Fence 282, 2012-2018, 1998
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Species: Caenorhabditis elegans
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vrossion: T18755
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peries: Caenorhabditis elegans
ate: 15 out:1999 #sequence_revision 15-Out 1900 #text_change 15-Out-1900
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ross references: EMBL.272824, FIDW.CAB07310.1, CESE:B0413.7
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                                                                          102 AIMEDDENEEP 112
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A;Molecule type: DNA
A;Residues: 1-330 <STO>
A;Coss-references: GB.AFC01512; GB BACCCOP4, MID 3]0124000, FIRE BAFCCCA
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                          spore cortex-lytic enzyme sleB [imported] - Racillus halodurans (strain C-125) C;Species: Bacillus halodurans (c;Species: Bacillus halodurans (c,Dite: n1 Dec-2000 #sequence_revision 01:Dec-2000 #text_chinge 15-Jun-2001 C;Accession: G83853 # C;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, B.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317, 4331, 2000 # Complete genome sequence of the alkaliphilic bacterium Bacillus balodurans and (c A;Forter complete genome sequence of the alkaliphilic bacterium Bacillus balodurans and (c A;Pecession: G83853 # A;Accession: G83853
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184 PEEPTPYEEA 193
                                                                                                        16.5%; Score 46; DB Local Similarity 80.0%; Pred. No. 31; Pred. No. 31; Pred. No. 31;
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Search completed. January 24, 2003, 11:11:50 Job time: 17 secs

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p5777 cricetulus
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p372u mus musculu
c1056 chlamydomon
c372u4 macaca mula
p372ua mus musculu
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c372u3 venopus lae
p25367 bome sapien
c62807 sus scrofa
c190c2 mus musculu
c15542 synethocyst
p09922 mus musculu
c15544 bome supien
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ALIGNMENTS

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MEDIANE 21010696; FubMod 11116860;
Talemi S., Equebi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
"A novel plotein, ETH XD, interacts with Fib Bol XD and Fol
                                                                                                                                                           Prinjha R., Moore S.E., Vinson M., Blake S., Morrow F., Christie Michalovich D., Simmons D.L., Walsh F.S., "Inhibitor of neurite outgrowth in humans.";
                                                                                                                                                                                                                                                                                                                                                                                                   is JUN 2002 (Rel. 41, Created)
15 JUN 2002 (Rel. 41, Last sequence update)
15 JUN 2002 (Rel. 41, Last annotation update)
15 JUN 2004 (Reurite outgrowth inhibitor) (Mogo protein) (Poocen)
(Neuroendocrine specific protein) (MSP) (Meuroendocrine specific protein) (MSP) (My043 protein)
                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF051335, AAF01564.1; ---
EMBL, AJ242961; CAB71027.1;
EMBL, AJ242962; CAB71028.1; ---
EMBL, AJ242963; CAB71029.1; ---
EMBL, AF132045; AAD31019.1; ---
EMBL, AF132045; AAD31029.1; ---
EMBL, AF132046; AAD31029.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a liverse agreement (
                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                             Nat ur - 403:383 384 (2000).
                                                                                                                                                                                                                            SECUTIVOT FROM N.A. (TOOFORMS 1, 2 AND 3)
                                                                                                                                                                                                                                                                                                  NOBI TALID DECE,
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                     RIN4 OR NOGO OR ASY OF FINADERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MQCY, 074762, Q9H212, Q9H313, QHKX35, QHYZY7, Q9UQ42, Q9Y233;
Q9Y5U6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIN4 HUMAN
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DOMAIN 1 989 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR0033BB; Reticulon.
Pfam; PE02453; Reticulon; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   623 SYDSIKLEPENPEPPER 640
                                                                            SUE Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYDSIKLEPENPPPYEEA 18
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3:
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192
1130
1163 AA;
                                                                                                                                                                                                                                                                                                                                       Metazoa,
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976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1131
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100.0%, Pred. No. 6.2e-07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               МW; 8СВ894ВОЧЕЧ4РПР6 СРС64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN ISOFORM 2).
MISSING (IN REF. 3; AAD31020)
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Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PET, 1192 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleustomi;
i, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1163,
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Ε ΤΟ ΚΟΥ ΑΙΕΓΑΙΟ ΚΑΙ ΑΙΚΟΙ ΜΕΙ ΑΙΚΟΙ ΚΑΙ ΕΙΚΟΙ ΕΙΚΟΙ
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N. A. (ISOFOPM 3).

MEDLINE:2049987, PhibMod 11042150;

Zhang Q. H., Ye M., Wu X. Y., Ren S. X., Zhao M., Zhao C. J., Fu G.,

Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X. R., Han Z.-G., Zhang J. W.,

Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen Z.,

"Cloning and functional analysis of cDNAs with open reading frames (o)

300 previously undefined g-mes expressed in CDN4+ hematopoietic

stem/progenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T , Ishikawa K -I , Suyama M , Kikuno R , Hirosawa M , Miyajima N , Tanaka A , Kotani H , Nomura N , Chata C , Miyajima N , Tanaka A , Kotani H , Nomura N , Chata C , Pata C , Statistical of the coding sequences of unidentified human genes. All The complete sequences of 100 new cDNA clamps from brain which code for large proteins in vitro.";

DNA Res  5.355-364 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jin W.-L., Ju G.; "Developmentally-regulated alternative splicing in a novel Mogo A."; "Developmentally-regulated alternative splicing in a novel Mogo A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R \gamma submitted (NOV-2000) to the EMRI/GenRank/PORG databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Song H., Peng Y., Zhou J., Huang Q., Dai M., Mac Y.M., Yu Y., Xu X., Luo B., Hu R., Chen J., "Human neuro-infortine-specific protein C (NSP) homolog gene.", submitted (JUL-1938) to the EMBL/GenBack/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE:20237542, PubMed=10773680; Yang J., Yu E., Bi A.D., Zhao S. Y.; Yang J., Yu E., Bi K.D., Zhao S. Y.; Yang J., Yu E., Bi K.D., Zhao S. Y.; Yang J., Yu E., Yang J., Ya
SECURICE OF 186-1190 FROM N A
                                                                                      Mao Y M , Xie Y , Zheng Z H.,
Submitted (MAY-1999) to the EMBL/JenBank/1988 databases.
                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                             SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
                                                                                                                                                                                                                                                                                                                         Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain, Pancreas, Placenta, and Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99156230; PubMed=10048485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N A (ISOFORM 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Novel human con
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Gu J.P., Wan E.F., Chan X.T., Chan X.M., Jiang H.Q., Chang P.P.,
Jin W., Huang Y., Qiu X.F., Qian E.F., He E.P., Li H.N., Yu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE EPOM N.A. (ISOPOPM 3)
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yutsudo M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N A. (ISOFORM 4)
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MEDLINE:20237542, PubMed=10773680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endoplasmic reticulum and reduces their anti-apoptotic activity.";
Ondegene 13-5736-5746(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rīssue-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human cDNA clone with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                         10:1546-1560(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the reticulon gene
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EMBL; AJ251383; CAB99248.1; --
EMBL; AJ251385; CAB99250.1; --
EMBL; AJ251385; CAB99250.1; --
EMBL; AJ251385; CAB99250.1; --
EMBL; AB040462; BAE18927.1; EMBL; AB040463; BAB18928.1; --
EMBL; AF148537; AAG12205.1; --
EMBL; AF148538; AAG1177.1; --
EMBL; AF087901; AAG12205.1; --
EMBL; AF087901; AAG12205.1; --
EMBL; AF132047; AAG31022.1; --
EMBL; AF132048; AAG31022.1; --
EMBL; AF087963; BAA83712.1; --
EMBL; AB017639; BAA83712.1; --
EMBL; AB017639; BAA83712.1; --
EMBL; AB017639; BAA83712.1; --
EMBL; AB017639; BAA74909; 1; --
EMBL; BC001035; AAH01035.1; --
EMBL; BC007109; AAH07109.1; --
EMBL; BC007109; AAH07207.1; --
EMBL; BC007109; AAH07209.1; --
EMB
                                                                                                             Endoplasmic reticulum; Alternative splicing; Transmembrane.

DOMAIN 1 1018 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF125103; AAD39920.1; ALT_FRAME EMBL, AF0636C1, AAD39920.1; ALT_INIT. EMBL; AF333336; AAN20831.1; ALT_INIT. Genew. HGMC.1408e. ETN;
                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reticulon protein ";
Nature 403:439-444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20129259, FubMed-10667797;
GrandPre T. Nakamira F., Vartanian T., Strittmatter S.M.,
"Identification of the Nogo inhibitor of axon regeneration as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sha J.H., Zhou Z.M., Li J.M.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific.
SIMILARITY: CONTAINS 1 RETICUTION DOMAIN.
CAUTION: Ref:11 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        after binding and sequestration.

SUBUNIT Interacts with Bcl-xl and Bcl-2.

SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains.

ALTEPNATIVE PRODUCTS: 4 isoforms: ILRIV 4A/ROGO-A/RIN-xL (shown here), 2/RTN 48/NOGO-B/RIN-xS/FOOCEN-M, 3/RTN 4C/NOGO-C/FOOCEN-here), 2/RTN 48/NOGO-B/RIN-xS/FOOCEN-M, 3/RTN 4C/NOGO-C/FOOCEN-MEMBRANE ACCORDANCE ACCORDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S and 4; are produced by alternative splicing.
TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain and testis and weakly in heart and skeletal muscle. Isoform 2 is widely expressed excepted for the liver. Isoform 3 is expressed in brain, skeletal muscle and adipocytes. Isoform 4 is testis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K04475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frameshifts in positions 1149 and 1156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION. Forest sourite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults.
                                                                                                                                                                                                                                                                              PF02453, Reticulon, 6.
PE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF125103; AAD39920
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LUMENAL (POTENTIAL)
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                                                  Query Match
                                       Best
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                                                                                                            EMBL; M27693; AAA46268.1; ...
PIP; A32592; ZNXPLC.
InterPro; IPR000822; Znf C2H2.
InterPro; IPR003224; Znf Pl1.
ProDom; PD020016; Znf Pl1; 1.
Pp05TTE; P500028; ZINC FINGER_C2H2_1; 1.
                                                                           SEQUENCE 90 AA; 10184 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990
01-NOV-1990
01-FEB-1991
                                                                                           Zinc-finger; RNA-binding.
ZN_FING 32 53
                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                      a unique RNA structure and a gene for a zinc finger protein." Virology 173:1-10(1989).
                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: MIGHT BE AN RNA-BINDING PROTEIN WITH A REGULATORY ROLE.
                                                                                                                                                                                                                                                                                                                                                               "The completed sequence of
                                                                                                                                                                                                                                                                                                                                                                            Salvato M.S., Shimomaye E.M.;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDUINE=90051057; PubMed=2510401,
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc finger protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZNFP_LYCVA
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymphocytic choriomeningitis virus (strain Armstrong)
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                                     Local Similarity
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5 IKLEPENPPPYEE 17
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                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1192 AA; 129930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 16, Created)
(Rel. 16, Last segmence update)
(Rel. 17, Last annotation update)
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1005
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186
107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                       atement is not removed. Usage by and for commercial license agreement (See http://www.ish.sib.ch/announce/
                                  48.5%; Score 49, DB 61.5%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.9%;
                                                                                                                                                                                                                                                                                                                                                           lymphorytic choriomeningitis virus reveals
                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM 4)
MISSING (IN ISOFORM 2)
S -> C (IN REF. 6)
E -> Q (IN REF. 6)
S -> P (IN REF. 1)
N -> S (IN REF. 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85; DB 1;
Pred. No. 7.6e-05;
                                                                           D25AF9EC2287E4EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAALQETEAPYISIAC -> MQLFKKQKLLIYLLHV (IN REF. 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN
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CYTOPLASMIC (POTENTIAL).
RETICULON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN ISOFORM 3)
                                               DB 1, Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> MDGQKFJWFCF
                     4; Indels
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Вb

78 ISTAPSSPPPYEE 90

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Wood V. Gwilliam R. Hayles J. Baker S. Basham D. Rowman S. Browns D. Rowman S. Baker S. Basham D. Rowman S. Browns D. Rowman S. Chillingworth T. Churcher C. M. Gallas M. Connor R. Cronin A. Davis P. Feltwell T. Fraser A. Gallas M. Connor R. Cronin A. Davis P. Feltwell T. Fraser A. Gallas M. Gable A. Hanlis N. Hartis D. Hiddigs J. Hedgens G. Holloyd S. Hornsby T. Howarth S. Hurkle E. J. Hunr S. Jagels K. James K. Johns E. James M. Learher S. McDenald S. McLean J. Monory B. Manile S. McHall F. Murthy S. McDenald S. McLean J. Monory B. Manile S. Manile 
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Eukityeth, Pungi, Ar. myssta, Schizosacchatomycetes,
Schizosacchatomycetales, Schizosacchatomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yanagida M.;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Heat thouck protein ctil bomoleg.
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EMBL, DRS.107; BAA.22619.1; -. EMBL; AL949498; CAR19910.1; -. HESSP, PS.4041; 1A17; TPR. InterFro; IPR001440; TPR. PLAM; PPS. PLAM; PPS. TPR; P. CMAPT; SM0002B; TPR; P. CMAPT; SM0002B; TPR; P. CMAPT; CMCONS; TPP; Propest; Popeat.

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HXD3
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                                                                                                HSSP; P02833; ISAN.
InterPro; IPP001827; Antennapedia.
InterPro; IPP001827; HTH_repressr.
InterPro; IPP001356; Homeobox
Pfam; PF00046; Homeobox; 1
PRINTS; PR00025; ANTENNAPEDIA.
PPINTS; PP00024; HOMEOBOX
PFINTS; PP00031; HTHPEPPESSE.
Pr0Dom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HXD3_CHICK STANDARD: PRT; 413 AA. 093353.
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homeobox protein Hox-D3.
HXXD3_CR_HXXD-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
Homeobox; DNA-binding; De
Transcription regulation.
DNA_BIND 173 232
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Richtormatics and the EMBC wish a collaboration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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REPEAT
REPEAT
                                                       PROSITE; PSS0071; HOMEOBOX_2; 1.
                                                                                       SMART;
                                                                                                                                                                                                                                EMBL; AF067959; AAC19377.1; -.
                                                                                                                                                                                                                                                             entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             development."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searcy R D , Yutzey K.E.; "Analysis of Hox gene expression during early avian heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria, Aves, Mangharhae, Gallifirmes, Phisianitae, Fhasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                           PROSITE; PSO0032; ANTENNAPEDIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                          · !- SIMILARITY: RELONGS TO THE ANTE HOMEOROX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 SADSAKFETTNPFFQFQA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                          PUDCTION: SEQUENCE-SECUTER TRANSCRIPTION FACTOR WHICH IS FART
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SERVIFUS PRISITUALS LICENTITIES OF THE ANTERIOR FISTEFICK AXIS.
SUBCELLULAR LOCATION: Nuclear:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Dyn. 213:82-91(1998)
FINCTION: SECUENCE-SE
                                                                                    SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .98401939, PukMed-9733103;
P D , Yutzey K.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 AA,
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103
298
331
372
432
466
500
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65544 MW, DZIMEDDDSMR4B4AA CRC64,
                           Developmental protein, Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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Fred. Mc. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPR 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1, Length 591;
                                                                                                                                                                                                                                                                                      Usage by and for commercial
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                SEQUENCE
                                                                                       DOMAIN
                                                                                                      Transcription regulation.
DOMAIN 78 137
                                                                                                                                                                                                                                                                                                                    InterPro; IPR901827, Antonnapedia.
InterPro; IPR000047; HTH repressr.
InterPro; IPR001356; Homeobox.
Pfam; Pf00046; homeobox, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC015180; AAH15180.1;
                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:5104; HOXA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC004079; AAB97950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: RELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION- SEQUENCE SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSITERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones K., Hinds K., Hawkins M., Duckels G., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones K., Hinds K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox protein Hox-A3 (Hox-1E). HOXA3 OP HOX1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              043365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                              142954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F02833,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                T03318;
                                            443 AA;
                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 AA;
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                                                                                     031
                                            46368 MW;
        46.5%;
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    Score 46;
                                                             HOMEOBOX
                                                                                                      PRO-RICH
                                                                                ANTP-TYPE HEXAPEPTIDE.
                                        365C93E65CA8E8FE CRC64;
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    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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Length 443;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                     -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DRYELOPMENTAL STAGE: EXPRESSED IN A SPATIALLY RESTRICTED MANNER EMBRYOS 8.5 DAYS P.C., EXPRESSION IS LIMITED TO THE CNS WITH AN ANTERTOR BOUNDARY IN THE HINDERAIN AND EXTENDING FOSTERICRLY THROUGH CAUDAL REGIONS OF THE SPINAL CORD. THE SAME SPATIAL EXPRESSION IS SEEN IN EMBRYOS 9.5 TO 12.5 DAYS P.C.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE-88030407; PubMed-2444477,

Fainsod A., Augulewitsch A., Puddle F.H.;
"Expression of the murine homeo box gene Hox 1 5 during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The homeo domain of a murine protein binds 5' to its own homeo box."; Proc. Natl Acad. Sci. H.S.A. 83:9532-9536(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85024859; PubMed=6091896; McGinnis W., Hart C.P., Gehring W.J., Ruddle F.H.; McGinnis W., Hart C.P., Gehring W.J., Ruddle F.H.; "Molecular cloning and chromosome mapping of a mouse DNA sequence homologous to homeotic genes of Drosophila."; Cell 38:675-680(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fainsod_A., Bogarad L.D., Ruusala T., Lubin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 185-258 FPOM N.A Ruddle F.H., Hart C.P., McGinnis W., "Structural and functional aspects o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruddle F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87092283; PubMed=2879282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96333206; PubMed=8710855;
Tan D., Shao X., Pu L., Guo V., Nirenberg M.;
"Sequence and expression of the murine Hoxd-3 homeobox gene.";
Proc. Natl. Acad. Sci. U S.A. 93-8247 9252(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 185-258 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homeobox protein Hox-A3 (Hox-1.5) (MO-10).
HOXA3 OR HOXA-3 OR HOX-1.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frends Genet. 1:48-51(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 54-280 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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P02831, Q61197,
21-JUL-1986 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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                                                                                                                                                                                                                                                                       PIOL 124:125-133(1987).

PHOL 124:125-133(1987).

PHOLION: SEQUENCE SPECIFIC TRANSCRIPTION FACTOR WHICH IS EART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTEFF-P-POSITEFICE AXIS.

BINDS 5' TO ITS OWN HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DSIKLEPENPPPYEE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crothers D.M.,
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Interpres (PR001827; Antennapedia, Interpres) (PR001845; Howeshox, Ptam, PR001845; Howeshox) (PR001845; Howeshox) (Pram, Pr00184; Howeshox) (Pr00184; Howeshox) (Pr00184; Howeshox) (Pr00184; Howeshox) (Pr00186) (Howeshox) (Howesh
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Enkarysta, Motadasa, Shordata, Craniata, Vertebrata, Esteleostsomi,
Minmusalia, Eatheria, Exebutia, Sciuropathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                              Aperlo C., Pognonect P., Saladin R., Auwery J., Boulukos K.E.;
"MANA "Coring and characterization of the transcriptional activities
of the hamster peroxicule proliferator activated receptor Marran
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forexer men preliferation and temperar jamma (PPAR-gamma)
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FUNCTION: REFERENCE HAT BIND FEROXICAME BE CLEERATISE OF WAS A LIGAND, THE RESIDENCE AND FAITY ACTION ONCE ACTIVATED BY A LIGAND, THE FER ACTIVATED BY A LIGAND, THE FER ACTIVATION OF A FEATURE BURNER OF THE SERVE FOR ACTIVATION OF ACTIVATION OF FAITY ALICE FEY ESPICALLY THE FER XIO MAY ALL VALUE OF ACTIVATE AND ACTIVATION AND ACTIVATE BUILDING OF ADDITIONAL OF FAITY ALICE FEY ESPICALLY OF ADDITIONAL OF FAITY ALICE FOR YOUR OFFERNAL BAILDY AND SUPPLYS BURNEVERSIES.
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356390; AA 52778.1;
K51591; AAA37512.1;
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015-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16 oct 2001 (Rel 40, Last innotation updat
the oct 2001 (Rel 40, Last innotation update)
RABIT
PPAT_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for the partities requires a license agreement (see http://www.isb.sib.ch/unnounce/or send an email to license.isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-New Zealand white; MECLINE-27419278, Fublication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI
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Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peroxisome proliferator activated receptor gamma (PPAR gamma) ppape op NP103.
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- - SUBSTRUCTURE UPCATION: Nuclear.
- - - SIMILARITY: RELUNCO TO THE NUCLEAR BURNOUR KROERIUK FAMILY.
MET SUBFRMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orymholagus cumiculus (Babbit)
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InterPro: IPRA01723; Stdhrmn_receptor.
InterPro: IPRC01628, Znf_C4steroid.
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3; Mismatches
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PRATZI; O14515; Q15178; Q15174; Q152; ONOR44; Q15140; Q00710;

O1-QCT-1994 (Rel 30, Created)

16-OCT-2001 (Rel 40, Last segmence update)

15-UNN-2002 (Rel 41, Last annotation update)

PRECYISTO [YOLK]

PRATZISON [YOLK]

PRATZISON
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PRINTS; PR00309; STEPHCEMONEE,
PRINTS; PR0000047; STEPOIDFINGEP,
Pr0D0m; PR000005; Znf_C4steroid; 1.
                                                                                                                                                                                                               MEDLINE=97218249; PubMed=9065481; Midherjee R., Jow L., Croston G.E., Paterniti d. P. dr.; Mukherjee R., Jow L., Croston G.E., Paterniti d. P. dr.; "Identification, characterization, and tissue distribution of human peroxisome proliferator-activated receptor (PPAP) isoforms PPARgamma2 versus PPARgamma1 and activation with retinoid X receptor agonists and antagonists."; "J. Bi-1 Chem. CTC scriptoral space (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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PROSTITE POCCOTI, WHOLEAR RECEPTOR, 1.

Receptor: Transcription regulation, Activator; DNA-binding,
Nuclear profein; Cinc-fingor, Milrigene family, Phosphorylation
NNA RIND 109 173 NUCLEAR RECEPTOR-TYPE.
SEQUENCE FROM M.A. (ISOFORMS 1 AND 2).
TISSUE-Fat body;
Elbrecht A. Chen Y. Cullinan C A., H
Moller D E., Berger J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eurheria; Primares; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECHRICE
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SMART; SMOO399, ZnF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPB000036, Hormone_rec_lig.
InterPro, IPB001723, Stdhrmm_receptor
InterPro, IPB001728, Onf_Q485eroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U84893; AAB96380 1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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PF00105; zf-C4; 1
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57.1%;
                                             Collinan C.A., Hayes M.,
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C4-TYPE.
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TISSUME-Placenta,
MEDLIME-9801012; PubMed=9356045;
MEDLIME-9801012; PubMed=9356045;
CRazawa H., Mori H., Tameri Y., Araki S., Niki T., Masugi J.,
Kawanishi M., Kubota T., Shinoda H., Kasuga M.,
Kawanishi M., Kubota T., Shinoda H., Kasuga M.,
"No coding mutations are detected in the percolsome proliferator-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kwan K., Hsieh L., Greene G., Nimer S.D.;
"Isolation of the human peroxisome proliferator activated receptor
gamma comA expression in hematogoletic colls and chromosomal
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Greene M.E., Blumberg B., McBride O.W.,
Kwan K., Hsieh L., Greene G., Nimer S.D.
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                                                                                                                                                                                                                                                                                                                                                                    MEDUINE-98086341, PubMed-9409061;
Yen C.-J., Beamer P.A., Negri C., Silvet F., Brown N.A., Yarnall D.
Burns D.K., Roth J., Shuldiner A.P.;
Burns D.K., Roth J., Shuldiner A.P.;
"Molecular scanning of the human peroxisome proliferator activated receptor gamma (hbpAR-gamma) gene in diabetic Caucasians:
identification of a proloala EPAF-gamma-2 missonse mutation.";
Blochem Biophys. Pes. Commun. 241-270 274(1997).
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                  VARIANTS COLON CANCER PRO-314 AND HIS-316, AND VARIANT ALA-12.
MEDLINE-99922672, FubMed-19394368
                                                                                            Hamann A., Munzberg H., Buttron P., Busing P., Hinney A., Mayer H. Siegfried W., Hebebrand J., Greten H., Gritted W., Hebebrand J., Greten H., Gritted W., Massense variants in the human peroxisome proliferator-activated receptor-garman Jens in lean and lease attents."
                                                                                                                                                                                                                                    Pistow M., Muller-Wieland D., Pfeiffer A., Frome W., Kahn C.B. "Obesity associated with a mutation in a genetic regulator of adipocyte differentiation.";
New Engl J Med 330.953-950(1998)
                                                                                                                                                                                                                                                                                                             VARIANT OBESITY GLN-113.
MEDLINE=98418646; PubMed=9753710;
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MEDLINE=20337987; PubMed=10882139;
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                                                                                                                                                                             MEDLINE=99337654; PubMed=10407229;
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                                                                              Endocrinol
NOOFTE, FURMEND-10394968
Mueller E., Smith W M
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PRINTS, PROBAG, STREBHORMONER.

PRINTS, PROBAG, STRENDERNIER.

PRINTS, PROBAG, STRENDERNIER.

PROBAG, PROBAG, STRENDERNIER.

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InterProj (PROUCS36), OldErna, rusep' i
InterProj (PROUCS36), Zuf (44) eroid
Plant (Proj) (PROUCS46), Zuf (44) eroid
Plant (Proj) (64), hormone rec; l.
Pfant (Proj) (65), zf (64), l.
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MIM; 604367;
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Scos M.A., Massec Ell, William T.D.M., Lewis H., Schafer A.J.,
Latternes V.E.K., Crahllly S.,
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80. 163415 BAA1894211;
80. 140044 AARO814.1;
80. 480-0542 BAA1893541; AUT INUT.
80. 480-05421; BAA233541; JOINED.
80. 480-05423; BAA233541; JOINED.
80. 480-05523; BAA233541; JOINED.
80. 480-05524; BAA233541; JOINED.
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CLICKACE INSPECTO IN PRAPT CAN LEAD TO TYPE 2 INCULIN-RESICTANT DIABETES AND HYPTERTENSION.
CLICKACE, DEFECTS IN PRAPT COULD PLAY A ROLE IN THE GENETIC PRESICULOSSITY.
CLICKACE, DESCRIPTION TO CHESSITY.
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Olby24; QMTQM6;
16-OCT-2001 (Pel. 40, Greated)
16-OCT-2001 (Rel. 40, Last segmence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Perovisome proliferator activated reverts galina (PPAR-gamma)
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                                                                                                                                                                                                                                                                                                                                             "Pelationships of PPAPyanna and PPAPyannan mEMA levels to obsainy diabetes and hyperinsulinaemia in rhosus monkoys."; Inc. J. Obes. Pelat. Metab. Disord. 22:1000-1010(1998).
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MCBI_TaxID 9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque).
Eukarycta; Metazca; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen B.C.
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Hotta K., Gustafson T.A., Yoshiok
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TISSUE=Adipose tissue;
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FUNCTION PROFITS THAT FIRE LEWING. THE TARGET AND ACTIVATED BY A LIGAMO, THE PROFITS TOWNS AND ENTRY ACTES COME ACTIVATED BY A LIGAMO, THE PROFITS TOWNS OF A PROMOTER ELEMENT IN THE GENE FOR ACTE ON A NAME AND ACTIVATED ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PROMISONAL BETA-OXIDATION FARIBACY OF FATTY ACIDS. KEY REQUIATOR OF ACTIVATION FOR ACTIVATION AND GROUNDSE HOMEOSTASIS.

SUBCELLULAR LOCATION: NUCLEAR FOR ACTIVATION X RECEPTOR.

SUBCELLULAR LOCATION: NUCLEAR FOR ACTIVATION X RECEPTOR.

SUBCULCUE INJURIES TOWNS OF ACTIVATION OF ACTIVATION AND COLORS OF ACTIVATION BETA-OCTOR. AT LEAST FIGURES. IN ACCIDENT METERS OF ACTIVATION BETA-OCTOR. AT LEAST FIGURES OF ACTIVATION AND COLORS.
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B - Y H (IN CO
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                                                                                                                                   TISSUE=Adipose tissue;
MEDLINE=95011336; Pubmed=7926726;
TONTONOZ P., Hu E., Graves R.A., Budavari A.I.,
"mPPAR gamma 2: tissue-specific regulator of an
Genes Dev. 8:1224-1234(1994).
MEDLINE=94059089; PubMed=8240342;
Chen F., Law S.W., O'Mailey B.W.;
"Identification of two mPPAR related receptors and evidence for the
                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=BALB/c; TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata,
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-00T-1994 (Pel 10, Created)
16-00T-2001 (Pel 40, Last sequence update)
16-00T-2001 (Rel 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                             Peroxisome proliferator activated receptor gamma (PPAR-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAT_MOUSE
P37238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC SEQUENCE
                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                      PPARG OF NRIC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: DPONGAR: STEDHORMOMER.
PRINTS: PROBOAT; STEDIFINGER.
PROBOM, FEGGEOGOSS: ZMF C48EFFFOID, 1.
SMART: SMO0430; TGF C4, 1.
SMART: SMO0430; ZGF C4, 1.
PPOSITE: PSONGSI: WTGLEAP FEGERTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD PES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPOSITE: PSOCODI: NFCLEAP FECEPTOR; i.
Receptor; Transcription regulation; Activator; DNA-binding;
Nuclear protein, Zino finger; Multigene family; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00104; hormone rec; 1. Pfam; PF00105; zf.C4, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR000536: Hormone rec lig. InterPro: IPP001723; Stdhrmn receptor. InterPro: IPP001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF033103; AAB87480.1; -.
EMBL; AF033343; AAB87482.1; -.
EMBL; AF033342; AB87481.1; -.
HSSP; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AIKVÉPASPPYYSE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [POGA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SIKLEPENPPPYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NR1 SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8,
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139
176
318
112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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57590 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 44 PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB
Fied. No. 18;
3; Mismatches
                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
MISSING (IN ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR RECEPTOR-TYPE. C4-TYPE. C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGAND BINDING (FOTENTIAL). PHOSPHORYLATION (BY MAPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41836A624AAF6942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 505;
                                                                                                                                                           Spiegelman B.M.; adipocyte enhanc
                                                                                                                                                           enhancer.";
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PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STRDHDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_PECEPTOR; 1.
Receptor; Transcription regulation; Activator; DNA-binding;
                                                                                                                                                    TWANNSAC: T02529; TWANNSAC: MGI: 97747; Eparg.
MGD; MGI: 97747; Eparg.
InterPro; IPR0001723; Stdhrmn_receptor.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone rec; 1.
Pfam; PF00105; zf-C4; T.
                                                                                                                                                                                                                                                                                                                                             EMBL; U09138; AAA62277.1; --
EMBL; U01664; AAA62110.1; --
EMBL; U01841; AAC52134.1; --
EMBL; U10374; AAA19971.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish.gib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOTINE TOWEST 97:2553-2561(1996).

-I- FUNCTION: RECEPTOR THAT BIND PERCHIFERATOPS SUCH AS HYPOLIFIEMED RUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE JENE FOR ACYL-COA CXIDASE AND ACTIVATES ITS TRANSCRIPTION IT THEREFORE COMPROLS THE PERCYSIONAL BETA OXIDATION FATHWAY OF FAITY ACIDS. KEY REGULATOR OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.

-I- SUBGUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.

-I- SUBGUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.

-I- SUBGUNIT: HETERODIMER WITH THE PRINCIP X RECEPTOR.

-I- SUBGUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.

-I- SUBGUNITI HETERODIMER WITH THE RETINOID X RECEPTOR.

-I- SUBGUNITI HETERODIMER WITH THE SUBGUNITY HERE); ARE PRODUCED BY ALIERNATIVE SPLICING.

-I- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE. ALSO FOUND IN LIVER, SKELETAL MUSCIE, HEAPT, ADRENAL GLAND, SELEEN, KIDNEY AND INCERBASES UNTIL BIRTH.

-I- DEVELOPMENTAL STAGE: IT APPEARS FIRST AT DAY 13 5 POSTCONCEPTION, AND INCERBASES UNTIL BIRTH.

-I- SIMILABITY: BEFORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to licensewish-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96249427; PubMed=8647948;
Vidal-Puig A., Jimenez-Linan M., Lowell B.B., Hamann A., Hu E.,
Spiegelman B., Flier J.S., Moller D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94086482; PubMed=8262913;
Zhu Y., Alvares K., Huang Q., Pao M.S., Red
"Cloning of a new member of the peroxisome
receptor gene family from mouse liver.";
J., Biol. Chem. 268:26817-26820(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94316694; PubMed=8041794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      existence of five subfamily members.";
Blochem. Biophys. Res. Commun. 196:671-677(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6 X CBA; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                    JN0881; JN0881.; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NR1 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELONGS TO THE NUCLEAR HOPMONE RECEPTOR FAMILY
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Heart Marie
                                                                Brshev A.V., Bazin N.J.;
"Phoroseceptor phagocytonic polectively activates PEARgamma expression refunct payment epithelial colls.";
In Represoi. Res. 60:328-337(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mayakita A., Shuko Si, Watababé T.K., Sya E
Suto T., Bakasawa K., Nakabara Y., Higashi E
"Molecular cloning of rat PPAR gamma gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feitkimp D., "Bastafsson C.A., Alexeon S.E.H.;
"Pat proxitions proliferator activated receptors and brown adipose tissue function adipose tissue function of a contraction.";

J. B.D. "Them "NATE DATE to contraction.";
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STRAIN Long Evans;
MEDILINE LORSINGTH; PubMed 1099535;
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lo ceT 201 (Bel. 48, Teat-1)
lo ceT 201 (Bel. 48, Last sequence update)
lo ceT 202 (Bel. 41, Last amost tilt update)
lo ceM 202 (Bel. 41, Last amost tilt update)
beroxisome proinferator activated receptor gamma (PFAE-gamma).
BBAB1 op HP104.
TOTAL STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE Adipocytes
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MELLIE 19367464; PubMed 19418514;
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"Town regulation of PPAP jammma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN Sprague Gawley; TISSUE Ádipose tissue;
Tanaka T., Itoh H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOWERS BY A TANK TO THE BOARD IN THE STREET
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Museulia, Butherna, Rodentin, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Particus convergences (Early
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5.35 AA;
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57.1%;
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MISSING (IN REF 2).

MY DR (IN REF 2).

MY S (IN REF 2 AND 4).

L F (IN REF 2).
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Pred. No. 18;
1; Mismatches 3; Indels
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C4-TYPE.
LIGAND-BINDING (POTENTIAL)
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K.,
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RT receptor gamma.",

RI J. Biol. Chem. 271:31771-31774 (1996).

Biol. Chem. 271:31771-31774 (1996).

CC -!- PRINCTION. RECEPTOR THAT BIND PERCONSOME PROLIFERATORS. JULY AND CC HYPOTION. RECEPTOR THAN EAST A PROMOTER PERCENT IN THE GENE POR ANYLOWA PROMOTER PERCENT IN THE SERVE ANYLOWA RECEPTOR RINDS TO A PROMOTER PERCONSOMAL HOTALWAY OF FAITH ANTON THE PERCONSOMAL HOTALWAY OF FAITH ANTON HEAD AND CONTROL THE PERCONSOMAL HOTALWAY OF FAITH ANTON HEAD AND CONTROL THE PERCONSOMER WHITH THE FRINGIS A RECEPTOR.

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                  Phosphorylation.
Phosphorylation.
Plus 129
ZN_FING 139
ZN_FING 176
POMAIN 318
                                                                                               Pfam; PR00105; Z1-5, ZFEHNEM-MER.
PFIMIS; FROUTH; STREINGER.MER.
PRODOM; FD000035; Znf_C4steroid; 1.
SMART; SM00436; Znf_C4, 1.
SMART; SM00339; ZnF_C4, 1.
PR0STTE: PS00031; NUCLEAR_EBCEPIOR; 1.
PR0STTE: PS00031; NUCLEAR_EBCEPIOR; 1.
PR0STTE: PS00031; NUCLEAR_BBCEPIOR; 1.
PR0STTE: PS00031; NUCLEAR_BBCEPIOR; 1.
PR0STTE: PS00031; NUCLEAR_BBCEPIOR; 1.
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MEDLING-97184167; PubMed-9038579;

Adams M. Reginal of 3. Shar D. Javar M.A. Charterjee V.K.;

"Transcriptional activation by perexisome proliferator activated team for Juneau is inhibited by phosphory action at a communication by position at a communication activated protein kinase position.";

J. Biol. Chem. 270 5128-5130 (1997).
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Pfam; PR00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                              InterPro; IPP000536; Hormone_rec_lig.
InterPro; IPP001723; Stdhrum; receptor.
InterPro; IPP0011629; Znf_Odsterroid.
Pfam; PF001104; hormone red; 1.
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White Cartington S., Gzalkowski D., Moller D.E.;
"Insulin- and mirogen-activated protein kinase mediated
phosphorylation, and activation of perodiseme proliferator acrivated
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Hu E., Kim J.B., Sarraf P., Spiegelman B.M.;
"Inhibition of adipogenesis through MAF kinase-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation of PPARgamma.";
Science 274:2100-2103(1996).
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Y12882; CAA73382.2;
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                                      WICLEAR RECEPTOR-TYPE C4-TYPE. C4-TYPE.
    FIGUREAU FINDING (FOTENTIAL)
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MUTAGEN
CONFLICT
SEQUENCE
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01-JUL-1993 (Pel 26, Last sequence update)
01-OCT-1993 (Pel. 27, Last ampotation update)
Flagollar radial spoke protein 4.
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Eukaryota: Viridiplantae: Chlorophyta,
Chlamydomonadaccae; Chlamydomonas.
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Mol. Cell Piol 12-296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-013r,
MEDLINE-003750(F, PubMed-1508107
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Yes 8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION FLAGELLAR PARTAL SPEYES CONTEXPOUTE TO THE PESULATION OF DYNEIN ARM ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING. THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBFIBER OF THE OUTER DOUBLET MISTORTHBUE, AND A PEUDOUS HEAD, WHICH IS ATTACHED TO THE STALK AND APPEARS TO INTERPACT WHITH THE PROJECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.

SUBULIT: THE PACIAL STOKE HEAD IS MADE OF FIVE DIFFERENT POLYBERIDES (PERL, PSP4, PSP4, AND PSP10).

CHECKLIAR LOCATION FACIAL SPOKE

SIMILARITY: TO THE FLAGELLAR PADIAL SPOKE PROTEIN 6.
                                                                                                                                                                                                                                                                                                      5 IKLEPENPPPYEEA 18
                                                                                                                                                                                                                                                                                                                                                                                   h 45.5%, cimilarity 57.1%; 8, conservative
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112
111
111
605 AA;
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                                        STANDARD;
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Pred. No. 18;
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MISSING (IN ISOFORM 1).
S--A- INCEPEAGES ADTECCENTS ACTIVITY
A -> P (IN PEF. 3).
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                                        477 AA
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Organization, response element recognition, heterodimer formation with retinoid x receptor and activation by fatty acids.";

7. Steroid Picchem, Mr. Bi-1 47 65-73/1993).

7. PINDITION: PREBYTOF THAT BIMD PREDXISHME PROLIFERATORS SUCH AS EXTENSIVE CONTROL RATES AND FATTY ALIES. GATE ACTIVATES BY A LIAMID, THE RECEPTOR BIMDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA CXITASE AND ACTIVATES ITS TRANSFEITION. IT THEREFORE CONTROLS THE PERSONAL BETA CONTROLS THE PRIMARY OF FATTY ACIDS. MET FEGULATOR FRENCH THE PETINOID AND THE FEGULATOR OF ACTIVATE DIFFERENTIATION AND THOMSE HOPETON.

7. SUBJECTIVE PROMOTER WITH THE RETINOID X RECEPTOR.

7. SINGLE-THY, EXCATOR MAINLY IN ACIDS TISSUE AND KIDNEY.

7. SINGLE-THY, ENCATOR ADULT.
                                                                         P PFARE PRODUCTS RE-C4; T.

P PRINTS: PRODUCTS, STEPHCHMONER.

R PRINTS: PRODUCTS, STEPHCHMONER.

R PRINTS: PRODUCTS, INT. C4steroid; 1.

R SMART; SMO0439; INT. C1FAP FECEFTCP; 1.

R SMART; SMO0339; INT. C1FAP; FECEFTCP; 1.

R SMART; SMO0339; INT. FAP FECEFTCP; 1.

R SMART; SMO0349; INT. FAP FECEFTCP; 1.

R SMART; SMO0349; INT. FAP FECEFTCP; INT. FAP Ending: FAP FECEFTCP. TWA binding: MUCLEAR RECEPTCP. TWA binding: MUCLEAR RECEPTCP. TYPE.

T DNA BIND 113 133 C4-TYPE.

T ZNETING 113 133 C4-TYPE.

T ZNETING 113 133 C4-TYPE.

T DOMAIN 293 477 LIGAND-BINDING (FOTENTIAL).

T MOD_RES 87 PHOSPHORYLATION (BY MAPK) (BY
Query Match
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MEDILINE-93:91267; FubMed=1312391;

Dreyer C., Krey G., Keller H., Givel F., Helftenbein G., Wahli W.;

"Control of the peroxisomal beta-oxidation pathway by a novel family of nuclear hormone receptors.";

Cell 68:879-887(1992).
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01-007-1994 (Pel. 30, Last segmence update)
16-007-2091 (Rel. 40, Last annotation update)
Perexisome proliferator activated receptor gamma (PPAP-gamma).
                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC, T01354, -
InterPro; IPP000636; Hormone_rec_lig.
InterPro; IPP001733, Stdhrmn receptor.
InterPro; IPP001628; 2nf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; C42214; C42214.
HSSP; P37231; 1FM9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=94100165; FubMed-8274443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPARG OR NR1C3. Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00104; hormone_rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, M84163,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Xenopus peroxisome proliferator activated receptors: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopodinae,
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                                         477
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                                      AA;
                                      54055 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata,
Score 45;
                                                            SIMILARITY).
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                                         160F87A401CB7246 CRC64,
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th completed January 24, 2004, 11:10:51 The complete decidentary 24, 2004, 11:10:51 The complete decident decidence and the complete decidence and the compl	Fer to earl Stmillarity 52.1%; Pred. No. 24; colors 9; Conservative 9; Mismatches 3; 4 SIKLEPENPPPEE 17
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Sp_archea:*

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Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the roral score distribution.

SUMMARIES

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4-	50	л Э	442	ر.	<u> </u>	Q51880 phormidium
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12	47	47.5	157	4	076025	076025 homo sapien
3	47	47.5	?		C927267	29uzs7 pyrococous
14	47	47.5	275	4	Q981:77	Qobu77 homo sapien
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ALIGNMENTS

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)	Ptam; PF00105; ZT-04; 1 PRINTS; PR000047; ZTP01DFINGER. PriDom: PD00014; Znf C44feroid: 1	ppnn104; hormone_rec; :	InterPro, Irrevesso, mainter recling.	31; 1FM9	AU249080; CAR51396.1;	EMBE, AJ249079, CABSIA96.1, JOINED	A/1249077; CAB51396 1;	AJ249076; CA851296.1;	L; AJ249075; CAB51396.1;	SIMILARITY	sassestand (Anti-type) of the Emph/Gensank/Dubin detabases.	L •	"A peroxisome proliferator-activated receptor gamma gene from a marine	.J.;	SEQUIENCE FROM N A	[1] -	NCBI TaxID=8262;	Pleuronectoidei, Fleuronectidae; Fleuronectes.	Additioned Pyli: Neopediyyli, teresetti, raterasetti, meoceteosetti		Pleuronectes platessa (Plaice).	PPAR.	proliferator-activated	(TremBirel, 21, Last annotation upda	(TrEMPLrel 12, Last	01-NOV-1999 (TrEMBLrel. 12, Created)	OWWOLD EXHLUMENT, EXT, NOT AA.	

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Covry Match
Best Local S
Mitches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00104; hormone_Fie; 1.
Pfam; PFC0104; if C4; 1.
PF00104; if C4; 1.
PF000047; STROHORMONEP
PFINTS: PF000047; STROHORMONER.
PF0000m; PF0000035, Inf C4steroid, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBG, AU241956, CARSIG18.1, HSSP, P47231, 1FM9.
Interpret 1PP000545, Hormone reciling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pleuronectes platessa (Plaice);
Bukuryeta, Medazet, Chordata, Carmiata, Vertekrata, Butelesstmi,
Actimopterygii; Mempterygii; Telecstei; Euteleostei; Neoteleostei;
Acamithomorphia, Acamithopterygii, Percomorpha, Pleuronectiformes,
Pleuronectoidei; Pleuronectidae; Pleuronectes.
                                  T04B1.4 protein.
                                                                0) AU3 1598 (TrEMBLE). 07,
0) AU3 1598 (TrEMBLE). 07,
0) MAR 2002 (TrEMBLE). 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marine fish."
Tarmorbabilitis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SMOO399; ZDF C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001723; Stdhrmm_receptor.
InterPro; IPR001628; Znf_MasTeroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUS 1956) to the EMBL/GenBank/DDRJ databases
t Submitted (AUS 1956) to the EMBL/GenBank/DDRJ databases
t SIMILARITY: HELDES, In THE MICHEAR HERMINE RESERVES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A peroxisomal proliferator activated receptor gamma gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leaver M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI _Tax1D-8262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peroxisome proliferator-activated receptor gamma.
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9) MAY 2000 (TrEMBLIE). 13, Last sequence update)
9) JUN 2002 (TEMBLIE). 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA binding; Nuclear protein; Receptor; Transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 HNSIKMEPESPPQYSDS 113
                                                                                                                                                                                                                                                                                                                              2 YDSIKLEPENPPPYEEA 18
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 AA; 60513 MW; DD3955E777961300 CRC64;
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                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 1:
Pred, No. 0.74;
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Pred. No. 0.73,
C. Mismathhas C. Indels
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                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                2957 AA
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RESULT 4
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Best Local
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Pfam; PF00176; SNF2 N; T.
SMART; SM00487; DEXOC; 1.
SMART; SM00487; HELLOC; 1.
SMART; SM00490; HELLOC; 1.
SMART; SM00395; SANT; 1.
PROSITE; PS50011; OHPOMO_2; 2.
PF0SITE; PS50010; MYB 3; 1.
ATP-binding; Helicase.
SEQUENCE 2957 AA, 325734 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Burton M., Burton M., Connoll M., Copey T., Coulson A. Craxton M., Dear S., D., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mottimere B., O'Callaghan M., Layd C., McKen L., Roopia A., Saunders D., Shownkeen F. Smaldon N., Smith A., Sonnhammer B., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudin M., Waterston R., Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P., Callaghan K., Waterston R., Callaghan K., Waterston R., Callaghan K., Waterston R., Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P., Callaghan K., Waterston R., Callagha
                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Davidson S , Wohldmann P.;
"The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metarda, Nematoda, Chromadotsa, Fbakkitika, Fbakkitoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                          NRTA-PHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The sequence of C. elegans cosmid T04D1.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                            STRAIN=OH-1-P-CL1;
                                                                     SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=32059;
                                                                                                                                                                                        Bacteria; Cyanobacteria; Oscillatoriales;
                                                                                                                                                                                                                                 Phormidium laminosum
                                                                                                                                                                                                                                                                                                           Probable periplasmic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q51880;
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InterPro: IPR001005; Myb_UNA_Binding.
InterPro: IPR000330; SNF2_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF067617; AAC17559.1; .
InterPro; IPPnnnes; Chromo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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MEDLINE=94150718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 VKMEPEKPSPYQQ 476
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53.8%;
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wery Match
Dery Match
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 07, Last annotation update)
Allene oxide synthase (EC 4 2 1 92) (Fubber particle protein) (EPP)
                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
STRAIN-LINE 11591, TISSUE-STEM BARK;
MEDILIMF-05/24971, PubMod 770/1745,
Pan 7, Durst F., Werck Felchhart D., Gardner H.W., Cardra B.,
Cornich K., Backhaus P.A.;
"The major protein of guayule rubber particles is a cytochrome
Characterization based on cDNA cloning and spectroscopic analys
the solubilized engyme and its reaction products.";
J., Biol. Chem. 270 8487-8404(1935).
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MEDLINE-95375238, FubMed-7647306,
MEDLINE-95375238, FubMed-7647306,
Merchann F., Kindle K.L., Llama M.U., Serra J.L., Fernandez E.;
"Cloning and sequencing of the nitrate transport system from the
"Cloning and sequencing of the nitrate transport system from the
"Cloning and sequencing of the nitrate transport system from laminosum:
"Charmophilic, filamentous cyanobaccorium Pharmidium laminosum:
"Charmophilic analysis with the homologous system from system from Synaphonogous system from Synaphonogous system from Synaphonogous specification.",
"Plant Mol. Biol. 28:759-766(1995).
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[2]
SEQUENCE FROM N A
STRAINSCHOLE CUL;
Merchan F CUL;
Submitted (JAN-1993) to the EMBL/G-nRink/DEBJ databases
SEQUENCE OF 122-160, 363-368 AND 407-421 MEDITHE-99325016; PubMod-9660772; PabMod-9660772; Pan Z., Camara B., Gardnor H.W. Backhau "Aspirin inhibition and acetylation of ri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TaxID 35035,
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CCE 442 AA; 47719 MW; 76A0FD8409536EF8 CRC64;
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                                Rackhaus P A
of the plant cytochrome
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       P450
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RESULT
RX MEDLING-20056006; PubMod:10731132;

RX MEDLING-20056006; PubMod:10731132;

RA Amanarides P G, Scher-1 S E, Li F W, Hockins R A, Galle R.F.,

RA Amanarides P G, Scher-1 S E, Li F W, Hockins R A, Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G G, Wortman J P., Vandell M D, Zhang Q, Chen L X.,

RA Hrandon P.C., Rogors Y - H.C., Blazed P G, Champe M, Peliffer B.D.,

RA Hardon P.C., Rogors Y - H.C., Blazed P G, Melson C.R., Millos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Raldwin D.,

RA Ballew P.M., Benos P.V., Bernan B.P., Ehadari D., Belshakov S.,

RA Horkova D, Bonchan M.R., Bouck J., Rocksein P., Brottier P.,

RA Horkova D, Bonchan M.R., Bouck J., Brokseein P., Brottier P.,

RA Horkova D, Bonchan M.R., Bouck J., Brokseein P., Brottier P.,

RA Horkova D, Bonchan M.R., Bouck J., Bavenport L.E., Davies P.,

Cherry J.M., Cawleys S., Dahlke C., Davenport L.E., Davies P.,

RA Pholos B., Delcher A., Dang C, Mays A D, Dow I, Diora S.M.,

PA Horston Y J., Boungelista C., Ferrar C., Ferriera S., Dillow B.C.,

PA Horston E, Couplista C., Ferrar C., Ferriera S., Fleischmann W.,

PA Horston E, Gong F, Govrell J.H., GH Z, Guann P., Harris M.,

PA Horston D, Houston K.A., Howland T.J., Wei M.-H., Ilegyaam C.,

PA Horston D, Houston K.A., Howland T.J., Wei M.-H., Ilegyaam C.,

PA Link Y, Levitsky A.A., Li Z, Li Z, Kennison J.A., Ketchym K.A.,

PA Merkulov G, Milshina N.V., Mcharry C, Morris J., McPhorson D.,

Marke E, Lei Y, Levitsky A.A., Li Z, Li Z, Marke E, Li Z, Marke E, Lei Y, Levitsky A.A., Li Z, Li Z, Li Z, Marke E, Lei Y, Levitsky A.A., Li Z, Li Z, Marke E, McCalles B, McIntosh T.C., McCalles B, McCa
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Fukaryota; Metazoa, Arthropoda, Tracheara, Hexagoda, Insocta;
Pterygota; Neoptera, Endopterygota, Diptera, Brachycora, Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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01-MAY-2000 (TrEMBLrel
01-MAY-2000 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
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Pfam; PFOOO67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSOGORA; CYTOCHROME_P450; FALSE_NEG.
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415
473 AA,
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415 E
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13, East sequence update)
21, Last annotation update)
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Pred. No.
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E -> EE (IN AA SEQUE
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STRAIN HERKELEY;
Stupleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stupleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Chimpe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mingall C.J.,
Nunco J., Facteb J., Paragas V., Park S., Phouanenaveng S., Wan K.,
Yu. C., Lowie S. F., Pubin G. M., Celniker S.,
Submitted (OCT 2001) to the EMBL/GenRank/DDRJ darabases
EMRL, ABO31768; AAF56847.1; ...
EMRL, ABO31768; AAF56847.1; ...
EMRL, ASO31429; AAL28977.1; ...
EMRL, ASO31429; AAL28977.1; ...
ENGO31429; AAL28977.1; ...
ENGO31429; FURIAD; ...
InterPro, IPR001737; RPNA A dimeth.
Pt.m. PECC3188; PrinaNJ, I.
Pt.m. PECC3188; PrinaNJ, I.
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⊱st Local S
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01 MAR 2002 (TEMMBLEE), 20, Created)

01 MAR-2002 (TEMMBLEE), 20, Last sequence update)

01 MAR-2002 (TEMMBLEE), 20, Last annotation update)

Bicarbonate transport bicarbonate-Finding protein
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                                                                                                                                                                                                                                                                                                                                MEDILINE 21595285; PubMed=11759840; Euroko T., Nakamura Y., Wolk C.P., Furitz T., Sasamoto S., Watanabo A., Iriquchi M., Ishikawa A., Kawashima K., Kimura T., Watanabo A., Iniquchi M., Matsawa A., Kawashima K., Kimura T., Kiubilda Y., Eubara M., Matsawata M., Matsawi N., Shimpo S., Sugimoro M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Yasuda M., Tabata S.;
                                                                                                                                                                                                                                "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain ECC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORYT49
                                                                                                                                                                                                        EMBL; AP003591; BAB74576.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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TE; PS01131; RRNA A DIMETH; 1
N.E. 306 AA, 35048 MW, CA0'
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                                                                                                                                      458 AA;
          Conservative
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                                                                                                                                      50292 MW;
49.5%; Score 49; DB 16; Length 458; 50.0%; Pred. No. 21; tive 3; Mismatches 4; Indels
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Fred. No. 14,
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                                                                                                                                          6A9903EBP60584EE ORO64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
      0
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د
      Gaps
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3

Q9USU2 ID Q9 RESULT 9

Q9USU2

PRELIMINARY;

PRT;

307 AA

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                                                                                                                                                                                                                                                                                                               InterPro; IPRO00719; Buk_pkinase.

P InterPro; IPRO03961; FN_III.

P InterPro; IPRO03961; FN_III.

P Ffam; pro0041; fn3; 1.

P Ffam; pro0041; fn3; 1.

P Ffam; pro0069; pkinase; 2.

P Pfam; pro0069; pkinase; 2.

P SMAPT; SM00408; IGC2; 1.

P SMAPT; SM00408; IGC2; 1.

R SMAPT; 
                                                                                                                                                                  Matches
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson P., Ainscough P., Anderson K., Haynes C., Berks M., Bunfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Craxton M., Dear S., Du Z., Durbin P., Favello A., Fulton L., Gradner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Fershaw J., Kirsten J., Laister M., Latreille P., Johnston L., Jier M., Johnston L., Jones M., Fershaw J., Kirsten J., Laister M., Latreille P., Jiehtning J., Eloyd C., McMurray A., More Ber G., O'Callaghan M., Lightning J., Eloyd C., McMurray A., Sanders M., Schwikeen Barsons J., Percy C., Pifken L., Poopes A., Sanders B., Schwikeen J., Smaldon N., Smith A., Sonnhammet E., Studen R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudin M., Waterston R., Waterston R., Wilkinson-Sproat J., Wohldman F., "2.2 Mb of contiguous nucleotide sequence from shromssame III of C. Belgans "100 and 100 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P91099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goela D., Wilson R.;
"The sequence of C. elegans cosmid C24G7.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBT databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C24G7.5 protein.
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01-MAY-1997 (TrEMBLrel. 03, Last seg-
01-MAP-2002 (TrEMBLrel. 20, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U88310; AAB42336.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FER-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368.32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metaroa, Nematoda, Chromadorea,
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C24G7.
1163
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                                                                             2 YDSIKLEPENPPPYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YESIKLEPENPEPY 15
YDYLRIQPKKPPPTVE 278
                                                                                                                                                              Conservative
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                                                                                                                                                                                                49.5%;
42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                    Score 49; DB
Pred No 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPT; 1398 AA
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                               DB 5; Length 1398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coulson A.,
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=KIDNEY;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0410010012Pik protein.
0410010012PIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00198; Frianc,
TIGRPAMS; TIGR00755; ksgA; 1.
PPOSITE; PS01131; RRNA A_DIMETH; 1.
mRNA processing; Transferase; Methyltransferase.
DOMALIN
28 21 POLY-PRO.
CONFLICT 170 170 S -> P (IN REF. 1).
CONFLICT 290 292 TEF -> QS (IN REF. 1).
CONFLICT 298 298 A -> P (IN REF. 1).
CONFILOT 298 298 A -> P (IN REF. 1).
CONFILOT 298 298 A -> P (IN REF. 1).
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DCT0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLDU60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001737; RRNA A dimeth.
InterPro; IPR000051; SAM_Bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES IN THE LOOP OF A CONSERVED HAIRDIN NEAR THE 3'-END OF 18S RRNA IN THE 40S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and comparative analysis of the SpDIM1 gene from Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9USU2; Q9Y7V3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-MC-2002 (TrEMBLrel. 21, Last annotation update)
01-MC-2002 (TrEMBLrel. 21, Last annotation update)
N'-ADENOSYL(PRNA) dimethyltrunsferase) (18S RRNA dimethylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL121815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z68293; CAA92585.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=972;
Borzym K., Beck A., Reinhardt R., McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIM1 OR SPEC336.02.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE RRNA ADENINE N-6-METHYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Housen I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharcmyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 IKLEPENPPP---YEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S -> P (IN REF. 1).
TEF -> QS (IN REF. 1).
A -> P (IN REF. 1).
VHFA -> RSFWLMGQDGVFH (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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OC OC OC OC
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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Podriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Synshaw-Boris A., Yoshida K., Hasegawa Y., Kawiji H., Kohtsuki S.,
RA Havasehiaki y. A., Yoshida K., Hasegawa Y., Kawiji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative dimethyladenosine transferase (Fragment)
                                                Homo sapiens (Human)
                                                                                                                                                      076025;
                                                                                                                                                                       076025
                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 125 AA; 14275 MW; 9E2E91518577BD01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrow I.K.-P., Boguski M.S., Touchman J., Spencer F., "Full-insert sequence of mapped XREF EST.", Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF091078; ACC72947.1; ... InterPro, TPR001737; ERNA_A dimeth. Pfam; PF00398; RrnaAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordara; Craniata; Vertebrata, Euteleustomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 14.3 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409.685-690(2001).

EMBL; AK002512; BAB22153.1, -...
MGD; MGI:1913310; 06100100012Rik.
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                                                                                                                                                                                                                                                                    19 VRIEPKNPPP 28
                                                                                                                                                                                                                                                                                                           5 IKLEPENPPP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TaxID=9606;
                                                                                                                                                                                                                                                                                                                                               6;
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                           47.5%; Score 47; DB 60.0%; Pred. No. 11;
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77.8%;
                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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Pred. No. 9.
                                                                                                                                                               PRT; 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 AA.
                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9;
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                                                                                                                                                                                                                            11 JUN(2.7) (THEMBLIE), 17, (Teated)
1 JUN(2.7) (THEMBLIE), 13, (ast sequence update)
1 JUN(2.7) (THEMBLIE), 13, last amoutation apdate)
1 JUN(2.7) (THEMBLIE), 13, last amoutation apdate)
1 JUN(2.7) (THEMBLIE), 1 JUN(2.1) (Transferase,
1 JUN(2.7) (THEMBLIE), 1 JUN(2.7) (Transferase,
1 JUN(2.7) (THEMBLIE), 1 JUN(2.7) (TH
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Interfers (PRO01737; REMA A dimeth.
Diag, PRO0183, Establic II
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Archaea, Buryas Lae ta,
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1 MAY Loop (TIEMHIJA). 13, 'teated)
2 MAY Loop (TIEMHIJA). 13, Last sequence update)
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6 MAC Loop (TIEMHIJA). 14, Last sequence update)
7 MAC Loop (TIEMHIJA). 15, Last sequence update)
8 MAC Loop (TIEMHIJA). 15, Last sequence update)
1 MAC Loop (TIEMHIJA). 15, L
                                                            DECUENCE PROMINIA.
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                                                                                                                                                                                                                                                                                                            Thurdata; Craniata; Vertebrata; Euteleostomi;
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Search completed: January 24,

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                                                            Matches
                                                                           Query Match
Best Local 9
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                                                                                                                                                                                              Strausberg R.;
submitted (001-2001) to the EMEL/Jenbaih/2050 databases.
EMPL; AP102147; AAC07055 1; -.
EMBL; BC010874; AAH10874.1; -.
Interpro; IPP001747; RPNA A dimeth.
Interpro; IPP001747; RPNA A dimeth.
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nl-MAY-2non (TrEMBLrel 13, Greated)

nl-MAY-2non (TrEMBLrel 13, Last segmence update)

nl-JUN 2002 (TrEMBLrel. 21, Last annotation update)

Putative dimethyladenosine transferace (Similar in putative
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EMBL, BC002841; AAH02841.1; -.
InterPro; IFR001737; ERNA A dimeth.
InterPro; IFR001737; ERNA A dimeth.
Pfonsos; IRN000051; SAM_Bind.
Pfam; PF00398; RINAAD; 1.
TIGPFAMS; TIGP00755; kegA; 1.
                                                                                                                                                                                                                                                                                                                                              Wei Y.J., Ding J.F., Liu Y.O., Xu Y.Y., Hui R.T., Sheng
Jiang Y.X., Liu D.Q., Zhao Y., Cao H.Q., Meng X.M., Liu
Submitted (OCT-1998) to the EMBL/GenBank/DDRJ databases
                                                                                                                          SEQUENCE
                                                                                                                                                   Pfam; PF00398; RrnaAD; 1.
TIGREAMS; TIGR00755; ksgA; 1.
PPOSITE; PS01131; PRNA_A_DIMETH; 1
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Mammalla; Eutherla; Frimates; Catarrhin; Hominidae; Homo.
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207 VRIEPKNPPP 216
                                                          Local Similarity
es 6; Conserv
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                            5 IKLEPENPPP 14
                                                                                                                                                                                                                                                                                                                                                                                             ECETA;
                                                                                                                      313 AA; 35236 MW; 306B9D4A4F9494A6 CRC64;
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                                                          Conservative
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                                                        47.5%; Score 47; DB 60.0%; Pred. No. 29; tive 4; Mismatches
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                                                                                          DB 4; Length 313;
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(., Liu S.;
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protein - protein search, using aw model
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Maximum Match
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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   طاراتانا طاطر طاطر طاطر واردان (c) (c) طاطر رازان) (مانيران) بران الإيارات
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 SUMMARIES
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Sequence 54, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 1, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli 
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PESHLT 2 US 09.494 2 Sequence Patent No Patent	Cuery Mate Rest Local Matches Cy 2 YD Db 180 YE	RESULT 1 US-09-537-54 Sequence 54, Application US/09 Patent No. 6271018 GENERAL INFORMATION: APPLICANT: Alan Brash APPLICANT: Nathalie Tijet TITLE OF INVENTION INASE AN FILE PEFEPEINE OF ON A ADSILUTION OF SEQUENCY TITLE OF SEQUENCE OF SEQUENCY OUPFENT FILLY DATE ON UNMARP OF SEQUENCY MINSER OF SEQUENCY ENGSTH: 405 TYPE: PRT OPGANISM: Guayule US-09-537-357-54		ממג שטשטי ב שטטען בבב בב מנכ אמט אד, מד מיים איט אמט מנכ אמט אד, מד מיים איט אמט
Sequence C, Application US Sequence C, Application US Patent No. 5861274 GENERAL INFORMATION: AFFLICANT: FORMAN, FAR AFFLICANT: COM, ESTELL AFFLICANT: ONG, ESTELL AFFLICANT: ONG, ESTELL AFFLICANT: ONG, ESTELL COMPRESEDNIENCES: FORTTY: UMBER OF ENQUENCES: E COMPRESEDNIENCE ADDRESS: AFFRESET: 444 SQUITH E CITY: LOS ANGELES STREET: 444 SQUITH FI COMPUTER FEADABLE FORM MEDIUM TYPE: F10PM	ch similarity 47	57-54 54, Applicat FORMATION: NFORMATION: T: Alan Bra T: Alan Bra T: WENT'ON FINEHTTON		41144 41144 41144 41144 41144 41144 41144 41144 41144 41144 41144
WELL VOHP VOHP VOHP VOHP VOHP VOHP VOHP VOHP	y 47 18, srvative 2PYEEA 18	រ ស ១៨ ហ		
4200 A. MILY AND HERS THERE DEEP, PRIPPORMANN S	Score 5i; PR 4; Lei Fred Da 6 5; 5; Mismatches 4;	37357 LOTERATE MELTE HYCEST LUSES THERFOR 1/194/537,357	ALIGNMENTS	US-08-732-751-12 US-08-236-886-1 US-08-732-751-7 US-08-732-751-7 US-07-596-081A-1 US-07-596-081A-6 US-07-596-081A-6 US-07-596-081A-6 US-08-723-425A-32 US-08-723-425A-32 US-08-723-425A-171 US-08-723-425A-171 US-08-723-425A-171 US-08-723-425A-171 US-09-112-206-171
CLVBA EOB CLVBA	ngth 405; Indels 0; Gaps	e E		Sequence 12, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 171, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli

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Lorry Match
46.5%; Score 46; DB
Hest Loral Similarity 57.1%; Pred. No. 30;
Mirchel 8, Colorinativ 3, Michaelthes
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APPLICANT: Forman, Barry M.
APPLICANT: Forman, Barry M.
APPLICANT: FOrman, Barry M.
FITTLE OF INVENTION. SELECTIVE MODULATORS OF PEROXISOME
TITLE OF INVENTION. USE THEREOF
FILE OF INVENTION. USE THEREOF
FILE REFERENCE: SALK1470-1
CURRENT APPLICATION NUMBER: US/08/465,375A
TURBENT FILIN: DATE. 1995-06-95
FARRILER APPLICATION NUMBER: 08/428,559
                                                                                                                  Application US/39764870 strent No. 6236946 strent No. 6236946 strent No. 6236947 strent No. 6236947 strent No. 6236947 strent No. 6236947 strent No. 623694 
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atom: No. 6022897
ENSPAL INFORMATION:
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MECHMATION FOR SEQ ID NO: 2:
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                                             APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US/JR/484,200
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hes Hy Conservative
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                                                                                                             Scanlan, Trace.
         Ragerer, John S
Fletterick, Robert J
Wasper, Richard D
Kushner, Peter J
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57.1%; Pred. No. 30;
rative 3; Mismatches
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US-08-980-115-10
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                                                          APPLICANT: Baxter, John D.
APPLICANT: Baxter, John D.
APPLICANT: Hetterick, Pobert J
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Kushner, Peter J.
APPLICANT: Moriletti, James W.
APPLICANT: West, Brian L.
APPLICANT: Shiau, Andrew K.
APPLICANT: Shiau, Andrew K.
TITLE OF HIVENTION: MICHERAR RECEPTOR LIGARIS AND LIGARID SHIBHING COMMING.
FILE REFERENCE UNAL 246/20US
CUMPENT APPLICATION NUMBER: US/08/980,1115
CURRENT FILING DATE: 1997-11-26
EARLIEP APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
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FILING DATE: 13-DEC-1995
PPIOP APPLICATION DATA:
APPLICATION NUMBER: U5 60/
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5 60/
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ATTORNEY/AGENT INFORMATION.
NAME: Makemmer.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1 0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA
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COMPUTER PEADABLE FORM:
TYPE: Floppy disk
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CORRESPONDENCE ADDRESS
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APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor
TITLE OF INVENTION: Binding Domains
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SLECOMMINION TOWNS 1972
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TOPOLOGY: li
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CITY: Palo Alto
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08-134-557D-2
08-134-557D-2
08-134-557D-2
Requence - Application U2/69134557D
REDELT - Application U2/69134557D
REDELTCANT Greene, Marianne E.
Applicant Greene, Marianne E.
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FARLLER FILLING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER 60/008,540
EARLIER APPLICATION NUMBER 60/008,540
EARLIER FILING DATE: 1995-12-13
NUMBER 0F SEQ ID NOS-17
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TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
FILE REFERENCE: SALK1480.2
CIPPENT APPLICATION MINORED TO 102-16
PRIOR APPLICATION MINORED TO 102-16
PRIOR APPLICATION MINORED TO 104/155, 102
PRIOR APPLICATION MINORED TO 104/155, 102
PRIOR FILING DATE: 1904-12-22
NUMBER OF SEC ID NOS: 7
SOFTWARE PAPONTIN VOYSION 1 0
EQ ID NO 2
LENGTH 475
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SPQ ID NO 10
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Patent No. 6413994
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APPLICANT: EVANS, F
APPLICANT: FORMAN,
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est Icon Similarity so 1%,
latches 8, Conservative
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LOCATION: (202) (47%)
OTHER INFOSMATION "finimal ligand binding demain
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                                                                APPLICANT: Greene, Marianne E.
APPLICANT: Blumberg, Bruce
TITLE OF INVENTION Human Peroxisome Froliferator Activated
TITLE OF INVENTION Peceptor Gamma. Compositions and Methods
NUMBER OF SEQUENCES: A
COPPESPONDENCE ACCESSES.
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ORGANISM Miss Missoilus
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ALL
SIPEET:
Cliv: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match
Local Cimilarity 40.5%, Score 46, 22 4,
Local Cimilarity 50 1%, Prod. No 30,
hos 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 AIKVEPASPPYYSE 88
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Pred No. 30,
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    Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/00170140
Fatent No. 6204559
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT. Smith, Roy G.
APPLICANT. Smith, Roy G.
TITLE OF INVENTION: ANTIPROLIFEFATIVE AGENTS ASSOCIATED WITH
PEROXISOME PROLIFEFATOR ACTIVATED FROEFFORE CLAMMAI AND GAMMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
TELEPHONE. (208) 594 530
TELEPAX. (208) 594 4720
INFCEMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORHEY/AGENT INFORMATION:
NAME: KALZ, MARTHIN L.
REGISTRATION UNMBER: 25,011
PEFERENCE/DOCYPT NUMBEP AP
TELECOMMUNICATION INFORMATION.
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ZIP. 60601
COMPUTEP PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY. linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECTENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUPPENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 57.1%; bes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IRM PO compatible
GPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PatentIn Release #1.0, Version #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Power Marintosh 7500/100
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER. US/09/128,142
FILING DATE: 03-Aug-198
CLASSIFICATION: <UNKnown>
FRIOR APPLICATION = AUR.
                                                                                                                                                                                                   AFFLICATION NUMBER 09/844,007 FILING DATE: <Unknown> ATTOENEY/AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                              TELECOMMUNICATION INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: April L Tribble
                                                                                                                                      NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: </
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey COUNTRY, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rahway
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                                                                                           (908) 594 5321
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Jequence 6, Application US/07614247A
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~9 514 247A 6
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(1) 182 4
(2) 183 182 4
(4) Performed 4. Application US/09128142
(4) Performed 10. 629459
(3) JENEFAL INFORMATION:
(5) CONTROLLING SMITH. ROY G.
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                                                                                                       105 AIKVEPASPPYYSE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION.
NAME: TIBBLE, Jack L.
NAME: TIBBLE, Jack L.
PEGISTRATION NUMBER: 32,633
PEGISTRATION NUMBER: SUnknown.
PERERENCE, SOCKET NUMBER: SUnknown.
TELEFOMMUNICATION INFORMATION:
TELEFOMMER: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AIKVEPASIFFYSE 95
                                                                                                                                               4 SIKLEPENPPPYEE 17
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PRIOR APPLICATION DATA:
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APPLICANT: Rmith, Roy G.
TITLE OF INVENTION. ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
PEROXISOME FROLIFEFATOR ACTIVATED FECEPTORS SAMMAL AND SAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLETULE TYPE: peptide
SEQUENCE DESCRIPTION, SEQ 15 NO. 2.
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                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO. 4.
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APPLICATION NUMBER: US/09/128,142
FILING DATE: 03 Aug 1998
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSPE: Jack L. Tribble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33
4.
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8; Combervative
                                                                                                                                                                                                               5.10.1.1.1.1.1.Y
                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 505 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: Power Macintosh 7500/100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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STPANDEDNESS: single
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                                                                                                                                                                                    Score 46; DB 4; Length 505; Fred. No. 32; 3; Mismatches 3; Indels
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Pred. No. 30;
3; Mismatches 3; Indels
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US-08-861-269-5
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Patent No. 5817494
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Bost Local Similarity 57.1%, Fred. No.
Matches 8, Conservative 3, Mismatch
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GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/00/514,247A CURPENT FILING DATE: 2000-02-28 PRIOR FILING DATE: 1908-08-24 PRIOR FILING DATE: 1998-08-24 PRIOR PRIOR PRIOR APPLICATION NUMBER: UF231084/1897 PRIOR PILING DATE: 1997-08-27 PRIOR FILING DATE: 1997-08-27 NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, TOMOYASU
APPLICANT: MIZUKAMI, JUNKO
TITLE OF INVENTION METHOR POF IDENTIFYING OF SCREENING AGENIST AND ANTAGONIST TO PFANILLE REFERENCE: TANIGUCHI=6
                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga APPLICANT: Corley, Neil C. APPLICANT: Lal, Preeti APPLICANT: Shah, Purvi TITLE OF INVENTION UPIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 506
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/A0 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
FREEPENCE/COCKET NUMBER: PR-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP. 94304
COMPUTER FEADABLE FORM:
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ADDRESSEE: Incyte Pr
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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CITY: Palo Alto
                                  STRANDEDNESS:
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                 TOPOLOGY:
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                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                  single
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Fred. No. 32;
3, Mismatches 3; Indels
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GENERAL INFORMATION:
APPLICANT: Bandwan, Olga
APPLICANT: Cerley Neil C.
APPLICANT: Lal, Procti
APPLICANT: Shab, Purvi
TITLE OF INVENTION: UPICHITIN CONSUMATION PROTEINS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equence 5, Application MS/09134596 atent No. 5922318
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INFORMATION FOR SEQ ID NO S
                          UT 13
9-293-273-5
                                                                                                                                                                                                                                                           TOPOLOGY: 1.
quence 5, Application US/09293273
tent No. 6057112
                                                                                                                                                                                  ery Match
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                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acid
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
ATTORNEY/AGENT INFORMATION:
NAME PILLINGS, LUCY J.
PROTSTRATION HUMBER: S6,743
PROTSTRATION HUMBER: PF C302 US
TELECOMMINUTATION INFORMATION.
TELEPHONE: 415 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEF: Incyta Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PPIOR APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: FOS
SOFTMARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA
APPLICATION NUMBER 12/11/114,572
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                                                                                                                                                        Local Similarity 80 0%;
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                                                                                            15 KIMVENPPPY 24
                                                                                                                                                                                                                                      CLONE: GenPank
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                                                                                                                        6 KLEPENPPPY 15
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                                                                                                                                                                                                                                                      397581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.4%; Score 44; DB 2;
90.0%; Pred Mo 30;
drive o, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635' : JB/ DU
                                                                                                                                                        Score 44, PB 2; Length 050,
Pred. No 30;
0; Mistathbes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 250;
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Patent No. 5859329
GENEFAL INFOFMATION
                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-379-556A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>118-09-293-273-5</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

PEGISTEATION UNMERE: 36,749

PEGEPENCE/DOCKET NUMBER. PF-OTELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEPHONE: 415-845-4166

INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
IMMEDIATE SOURCE:
***BBARY: 397581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, purvi
TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
NUMBER OF SECTIONS: 8
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEP: IEM PC COMPACTI
OPEFACTIVE SYSTEM PC-DOS.
                                                                                                                  CIPPEST MIDENCE ADDRESS:

ADDRESSEE SCILLY SCOTT MURPHY & PRESSER
STREET 400 GANDEN CITY FLAZA
CITY: GAADDEN CITY
STATE. NEW YORK
                                                                                                                                                                                                                APPLICANT: HOLTON, TIMOTHY A.
APPLICANT: KEAM, LISA A.
TITLE OF INVENTION. GENETIC SEQUENCES ENCOLING FLAVONOL
TITLE OF INVENTION. SYNTHASE ENGYMES AND USES THERREFORE
NUMBER OF SEQUENCES. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPERAPING SYSTEM. DOS
SOFTWARE: FASKSEQ for Windows Version 2 0
CUERENT APPLICATION DATA:
APPLICATION NUMBER: US/00/203,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBD1...
LIBRARY: 3>...
CHONE, GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS. sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Con
OPERATING SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 KLMVENEPPY 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 amino acids
                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.4%, Scare 44, DB 3, 80.0%, Pred. No. 30;
    compatible
FO-DOS/MS-DOS
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LEMNTH: 47 amino acids
TYPE: amino acids
TYPE: amino acid
Tydes(AST): linear
M Decree Type: protein
8 37) theA a
1.0-18 Att-3.
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TELEX: 280-001-880-10-99-12-8
SEQUEN'E HAPA TEPISTIN: 28-280-10-99-12-8
LEFTHE 447 amino acids
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ATTS PREY A BATTENE AND MARTICK:
MAMES DISTOLOGIES, FRANK S.
FIGHETRATION NUMBER 31,346
FIGHETRATION NUMBER 31,346
FIGHETRATION STRAITS N.
TELEFONE STRAITS N.
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CASSET NATE N. 933

ATTORNEY AGENT ING BRATION:
MARE DISTRICT, FRANK S.
FESTIVEFATION NUMBER: 9592

FESTIVET ATTORN NUMBER: 9592

TELEPHENE: (516)747, 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELLEPAX: ($16.742.446)
TELLEX: 70 901 SANS UP
TELLEX: 10 901 SEQ ID N 4
3.60/TEN E HARANTERISTINS:
TEN UH: 241 amino 1014s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7. V455 6.64 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VPCS 64.8
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TOPERT AFFILMATIN NATA: 
ASPILEATION NUMBER: US/08/379,456A 
ELLIN CATE: 22 MAR 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDICA TYPE: Floppy disk
- MEDICA: HEM PO compatible
- HEATID SYSTEM: PO DOS/MS DOS
- DEFWARE: Patent in Release #1.0, Version #1.30
- MEDICA: WINDOW NUMBER: US/04/479,656A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ** Addola : BAAL WILLEM: ** AMEDIAN *** AM
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TOWAY: (5157)...
O' CANS UR
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STY GARDEN STYY
STATE: NEW YORK
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15. – Autorios (2. jene
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400 GARDEN TITY PLAZA
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43.4%; Score 43; DB 2; Length 347;
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Search completed, January 24, 2003, 11.12:10 Job time: 16 secs

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imum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                               Score
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1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_c/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_c/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_c/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_c/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_c/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*

14: /cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
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                                      Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                   Query
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11 US-09-893-348-18
11 US-09-893-348-2
11 US-09-758-140-6
12 US-09-884-260A-54
12 US-09-884-260A-54
12 US-10-142-373-2
10 US-09-765-111A-16
12 US-10-109-866-6
12 US-09-765-111A-1
13 US-09-765-111A-2
14 US-09-765-111A-2
15 US-09-765-111A-2
16 US-09-765-111A-2
17 US-09-765-111A-2
18 US-09-765-111A-2
19 US-09-765-111A-2
19 US-09-765-111A-2
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10 US-09-765-111A-2
10 US-09-765-111A-2
10 US-09-765-111A-2
10 US-09-765-111A-4
10 US-09-765-111A-4
10 US-09-765-111A-4
10 US-09-765-111A-4
10 US-09-841-132-297
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                    Sequence 54, Appl
Sequence 2, Appli
Sequence 27, Appli
Sequence 16, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 23, Appl
Sequence 43, Appli
Sequence 6, Appli
Sequence 39748, A
Sequence 437, Appl
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Sequence 18. Appl
Sequence 2. Appli
Sequence 6. Appli
Sequence 6. Appli
Sequence 54. Appli
Sequence 54. Appli
Sequence 27. Appli
Sequence 27. Appli
        Sequence 431, App
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                          10 US-09-93-170-58
9 US-10-001-887-94
10 US-09-925-297-73
11 US-09-925-297-73
12 US-09-223-490-4
13 US-09-223-490-4
14 US-09-864-761-34248
15 US-09-864-761-34248
16 US-09-925-302-66
17 US-09-95-302-66
18 US-10-086-464-8
19 US-10-086-464-8
10 US-09-764-877-1159
11 US-09-764-877-1159
11 US-09-764-87-1159
12 US-09-925-306-1634
13 US-09-925-306-1634
14 US-10-174-596-376
15 US-10-174-596-376
16 US-10-175-737-376
17 US-10-175-737-376
   US-10-107-868-16
US-10-107-829-16
US-10-107-907-16
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US-09-865-960-2
Sequence 376, App
Sequence 376, App
Sequence 376, App
Sequence 376, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                          Sequence 8, Appli
Sequence 984, App
Sequence 1169, App
Sequence 36982, A
Sequence 1634, Ap
                                                                                                                                                            Sequence 58, Appl Sequence 94, Appl Sequence 738, App Sequence 4, Appli Sequence 4, Appli Sequence 482, App
                                                           Sequence 24, Appl
Sequence 24, Appl
                                                                                                                                                                                                         Sequence 244,
Sequence 2, F
                                                                                                                    Sequence 18, Appl
                                                                                                                                    Sequence 6, Appli
Sequence 34248, A
Sequence 1, Appli
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Appli
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ALIGNMENTS

RESULT 1 US-09-893-348-19

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APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TITLE OF INVENTION: ACTIVATED T-CRILS, MERVOUS SYSTEM-SIECIFIC ANTIGENS AND THEIR USE;
FILE RETERENCE: EIS-SCHMARTZ-2A
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/318,277
PRIOR APPLICATION NUMBER: DCT/US98/14715
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR APPLICATION NUMBER: IL 124500
PRIOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 18
TYPE: PRT
TYPE: PRT
                          RESULT 2
US-09-893-348-18
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Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH: SCHWARTE, Micha
APPLICANT: COHEN, Irun R.
APPLICANT: BESERMAN, Pierre
Sequence 18, Application US/09893348
                                                                                                                                                                                                                Matches
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nes 18; Conserv
                                                                                                                                            1 SYDSIKLEPENPPPYEEA 18
                                                                                                                    1 SYDSIKLEPENPPPYEEA 18
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MOSONEGO, Alon
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                               100.0%; Score 99; DB 10; Length 18; 100.0%; Pred. No. 3.4e-08; Indels
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Sequence 6, Application 78/09758140
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APPLICANT: PRINJHA, RABINDER KUMAB
TITLE OF INTENTION, NOVEL CONFOUNDS
FILE PEPERPENCE: GP-90165-C1
CORRENT APPLICATION NUMBER: US/09/789,186
                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 6 NUMBER OF SEQ ID NOS: 6
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19108 APPLICATION NUMBER: U.F. 9916898 1

PRIOR FILING CATE: 1939 07 13

PRIOR PAPELITATION NUMBER: U.E. 9816024.5

PRIOR FILING DATE: 1998 07-22

19108 APPLICATION NUMBER: US 90/159,208

PRIOR FILING DATE: 1999 07 22
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Watent No. US20020010324A1
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CITCLE OF INVENTION: ACTIVATED T CELLS, NERVOUS SYSTEM SPECIFIC ANTIGENS AND THEIR USB
FILE PREFERENCE: BIS SCHWARTZ-2A

TURRENT ALICINAL KUNNES, SC.L./H+8,348

TURRENT FILLING DATE: 2001-06-28

PFIOR APPLICATION MUMBER: US-09/214,161

PFIOR FILLING DATE: 1999-18-19

PRIOR FILLING DATE: 1999-18-22

PRIOR FILLING DATE: 1999-12-22

PRIOR FILLING DATE: 1998-12-20

PRIOR APPLICATION NUMBER: PCT/US98/14715

PRIOR APPLICATION NUMBER: PCT/US98/14715

PRIOR APPLICATION NUMBER: NCT-US-19

PRIOR PILLING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: NCT-US-19

PRIOR PILLING DATE: 1998-07-21
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                                                                                                                                                                                                                                                                                                                                                                          SPOANISM: HOMO SAPIENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NERAL INFORMATION.
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ORGANISM: Partus norvegious
9-893-349-18
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                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO :
                                                                                                                                   64% NYESIKHEPENPPPYEEA 662
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Local Similarity 100.0%; Score 99; DB 10; Length 1163;
Local Similarity 100.0%; Pred. No. 2.9e-06; Indels 0
                                                                                                                                                                                  1 SYDSIKLEPENPPPYEEA 18
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MOSONEGO, Alon
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Fred. Mo. 0.00027,
                                                                                                                                                                                                                                         Mismatches
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US-09-972-599A-6

Sequence 6, Application US/09972599A Fatent No. US20020077295A1

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-893-348-23
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EFICE APPLIATE NIMBER: 2000-01
EFICE APPLIATE NIMBER: 2000-05
PRIOR FILING DATE: 2000-05
PRIOR PILING DATE: 2000-05
PRIOR PILING DATE: 2000-05
NUMBER OF SEU ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
AFFLICANT:
APPLICANT:
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Patent No. US20020072493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US20020012965A1 GENERAL INFORMATION:
                                                                                      Query Match 85.9%; Score 85; DB 10; Length 1192; Best Local Similarity 83.2%, Fred. No. 0.00027; Matches 15; Conservative 2; Mismatches 1, Indels 1
                                                                                                                                                                                                                                                                               SEQ ID NO 23
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Best Local Similarity
Matches 15; Conserva
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FILE REFERENCE: 445073-US
CUEPFENT APPLICATION NUMBER: US/04/758,140
CURRENT FILING DATE: 2001-01-12
CURRENT FILING DATE: 105-60/175,707
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1098 12:22
FRIOR PRILING DATE: 1098-07-21
PRIOR PRILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUPPENT APPLICATION NUMBER: US/09/893,348
"TERENT FILLYS CATE 2002-6-29
PRIOR APPLICATION NUMBER: US 09/314,161
PPIOP FILING DATE: 1999-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MOALEM, GILA
TITLE OF INVENTION: ACTIVATED T CELLS, DERVOUS SYSTEM STEERING ACTIGENS AND THEIR USES
FILE REFERENCE: EIS-SCHWARTZ-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Strittm
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                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1192
TYPE: PRT
ORGANISM: Homo sapiens
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645 NYESIKHEPENPPPYEEA 662
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                                            1 SYDSIKLEPENPPPYEEA 18
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MOSONEGO, Alon
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WENTION: M5 "MSCC20C12965A1 Shower : Mc31 and 81 holds ( Ar hold Growth
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2000-05-26
WBER
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83.3%;
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Pred. No. 0.00027;
2; Mismatches 1; Indels
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APPLICANT STREAM NOTES STEPHEN M.

TITLE OF INVENTION NOTO-FECEPTOF-MEDIATED BLOCKADE OF AXONAL GROWTH

FILE REFERENCE: COT7 CIP IN:
CHERRENT APPLICATION NUMBER: HS/00/072,500A

CHERRENT APPLICATION NUMBER: HS/00/072,500A

PRIOR PILING DATE: 2001-01-12

NUMBER: 60/207,366

PRIOR PILING DATE: 2001-01-12

NUMBER: 60/175,707

PRIOR FILING DATE: 2001-01-12

SOFTWAPF: PILING DATE: 2001-01-12

SOFTWAPF: PILING DATE: 2001-01-12

SOFTWAPF: PILING DATE: 2001-01-12
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09-884-260A-54
eTHENTO 54, Application TS/OGS94260A
arent No US20020008570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION MODERATION (TUTUMIS MELT) HYDROSERONIGE
TITLE OF INVENTION. LYAKE AND USES THEREOF
FILE PEFFERNCE, 06027 OF OCCUP
CURRENT APPLICATION MUMBER. US/00/984,260A
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/,537,357
PRIOR APPLICATION NUMBER: 09/,537,357
PRIOR FILING DATE: 2000-03-29
NUMBER OF SECIE NOS: 56
NOFTMARE: FastSEQ for Windows Version 4.0
EQ ID NO 54
LENGTH. 400
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                                                                                                                               equence 2, Application US/10142373
Itent No. US20020137665A1
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CRGANISM: Homo sapiens
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0-142 373 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Guayule
PPLICANT: EVANS, RODAID

PPLICANT: FORMAN, BARRY

ITLE OF INVENTION: MODULATORS OF PERCXISOME PROLIFERATOR ACTIVATED

ITLE OF INVENTION: BECEPTOR GAMMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1192
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83.3%; Pred. No. 0.00027;
ative 2; Mismatches 1, Indels
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GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
TITLE OF INVENTION. FAX8 FFARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION. FAX8 FFARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION. AND PCLYPETTICES AND USES THEFFEOF
FILE PEREPROTE: BOROL/7196/EBP/MAT
TUFFENT AFFLICATION NUMBER: US/09/765,111A
CUTRENT AFFLICATION NUMBER: US/09/765,111A
CUTRENT FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-27
SPRIOR FILING DATE: 2000-01-27
SPRIOR FILING DATE: 2000-01-27
SPRIOR FILING TATE: 1000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWAPE: PASTSEQ for Windows Version 3.0
SEQ ID NO 27
LEMENTH: ATO
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, ORGANISM. Mus Musculus
US 10 142 373-2
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Best Local Similarity
Thicks 8; Conserve
                                                                                                                                                                                                                                                     ; Sequence 16, Application US/09765111A ; Patent No. US20020106796A1 ; GENERAL INFORMATION:
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LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
TITLE OF INVENTION: FAXA FFAFGATTA AND USES THEREOF
FILE REFERENCE: B0801/7105/ERP/MAT
CURRENT APPLICATION UNMEER: US/09/765,111A
CUPPENT FILING NATE: 2001-01-18
PRIOP FILING NATE: 2001-01-10
PRIOP FILING NATE: 2001-01-10
PRIOP FILING NATE: 2001-01-20
PRIOP FILING NATE: 2001-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPIOR APPLICATION NUMBER: US/09/788,070
PRIOR FILING DATE: 2001-02-16
PPIOR APPLICATION NUMBER: US 09/455,300
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF EILE REFERENCE: SALK1480-2
CUPRENT APPLICATION NUMBER: US/10/142,373
CUPRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 478
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 AIKVEPASPPYYSE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AIKVEPASPPYYSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SIKLEPENPPPYEE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.5%, Score 46; DB 10, 57.1%, Fred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 478;
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HENERAL INFORMATION.

APPLICANT: AVENTIS PHARMA S.A.

APPLICANT: AVENTIS PHARMA S.A.

TITLE OF INVENTISH TYPEM E A RESULATING IN VIV. THE EXERECSION OF A TRANSGENE BY
TITLE OF INVENTION. CONDITIONAL INHIBITION

FILE REFERENCE: 0.4806.0512

CURRENT FILING DATE: 2021 08.17
PRIOR APPLICATION NUMBER. FR 00/10710
PRIOR APPLICATION NUMBER. FR 00/10710
PRIOR APPLICATION NUMBER. FR 00/10710
PRIOR FILING DATE: 2000 08-18
PRIOR FILING DATE: 2000 08-18
PRIOR FILING DATE: 2000 10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09931007A
Satent No. US20020166132A1
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TITLE OF INVENTICAL METROE ES FICENTIFYTHS CS SCREENING AGONIST AND
TITLE OF INVENTICAL METROCNIST TO FPAR
FILE REFERENCE: TANICUCHE:6
TURPENT APPLICATION NUMBER: 05/15/159,896
TURPENT FILING DATE: 2002-04-01
FRICH APPLICATION NUMBER: 05/414,247
FRICH ETLING TOTE: 2000-02
FRICH APPLICATION NUMBER: 05/414,247
FRICH FILING TOTE: 2000-02
FRICH FILING TOTE: 2000-03
FR
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                                                                                                                               MUMBER OF SEC ID NOS: 11
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APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
                                                                           SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nery Match
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SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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FORTWARE, PASTSEC for Windows Version 3.6
FO ID NO 16
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9-765 111A-16
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AIKVEPASPPYYSE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 ALKVEPASPPYYSE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viesnoj in seq
Alabamoj in seq
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Similarity 57.1%; Fred. No. 30;
8; Conservative 3; Micmail
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TANIGUCHI, 10mc,
TANIGUCHI, 10mc,
Taniko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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US-09-931-007A-1
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                                                                                   SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application Ms/09765111A Patent No. US20020106796A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.5%; Score 46; DB Best Local Similarity 57.1%; Pred. No. 47; Matches 8, Conservative 3, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity 57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHREENT APPLICATION NUMBER: US/04/785,111A CURETH FILING DATE 2000-01-18 PRIOR APPLICATION NUMBER: US 60/177,109 FRIOR FILING DATE, 2000-01-20 FRIOR FILING DATE, 2000-09-14 PRIOR FILING FATE: 2000-09-14 NUMBER OF SEQ ID NOS: 47 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                  PRIOR FILING DATE: 2000-08-14 NUMBER OF SEQ ID NUS: 47
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/765,111A CURRENT FILING DATE: 2001-01-18 PRIOP APPLICATION NUMBER: US 60/177,109 FRIOR FILING DATE: 2000-01-20 FRIOR APPLICATION NUMBER: US 60/225,073
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FAX8 FFARGamma NUCLEIC ACID MOLECULES TITLE OF INVENTION: AND POLYPEPTIDES AND USES THERFOF FILE PEFFECCE B6401/7134/EPP/MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
TITLE OF INVENTICH: FAXA-FFAAGgamma NUCLEUC ACTE MOLECULES
TITLE OF INVENTICH: AND FOLYFEFTIDES AND USES THEREOF
FILE REFERENCE: BORG1/7136/ERP/MAT
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fletcher, Jonathan A. APPLICANT: Kroll, Todd G.
                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
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NAME/KEY: misc
LOCATION: (1)..
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo Sapiens
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OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-gamma
OTHER INFORMATION: eroxisome Proliferator Activated Federical gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                       LENGTH: 811
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Pred. No. 41;
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Op-765.111A-23

Derry Match

Ast Loral Similarity 47.1%; Score 46; DB 10; Length 811;

best Loral Similarity 47.1%; Pred No. 40;

Ast Loral Similarity 47.1%; Pred No. 40;

A SIKLEPENPPYEE 17

411 AINVERASPPYSE 424

411 AINVERASPPYSE 424

41 AINVERASPPYSE 424

42 APPLICANT; Broll Todd G.

APPLICANT; Broll Todd G.

TITLE OF INVENTION: AND POLYPEPTIES AND USES THEREOF

FILL BEFFERENCE. B060/17/109

PRIOR APPLICANTON NUMBER: US/09/765,111A

PRIOR APPLICATION NUMBER: US/09/765,111A
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items
Set
                Description
        2483
                NOGO
        143.
                S1 AND NEUR?
33
         214:
                S1 AND NEEV?
34
         51.
               S1 ANI CENTRAL(W) NERVOUS(W) SYSTEM
55
          36:
               FD (unique items)
               SS AND SPINAL(W) CORD
36
                AU- 'EISENHACH-SCHWARTZ MICHAL'
                AU-'HAUBEN, EHUD'
SS
S9
               AU='HAUBEN, E.'
$10
          9.
               AU- 'HAUBEN E'
           1 : AU= 'HAUBEN EHUL'
S11
          5.7
               AU='HAUBEN E.'
S12
          14 AU='COHEN, IRUN R'
S13
               AU= 'COHEN IRUN R'
S14
          11...
               AU='CCHEN I E.'
515
          80+
S15
          36.
                AU= 'COHEN I.F..'
SL^{\pm}
                AT= BESERMAN PIERRE'
SIE
                AU='MCALEM G'
           2 ·
               AU='MDALEM G.'
S13
SED
               AU='MOALEM GILA'
          1:
S21
                AU='MDALEM, GILA'
                MOGO AND S7 OF S8 OR S9 OR S10 OF S11 OR S12 OR S13 OR S14
522
              OR $15 OF $16 OF $17 OF $18 OR $19 OR $20 OR $21)
523
              ED (unique items)
334
          46
               NOGO AND SPINAL(W)CORD
               NO (unique items)
8335
          35 -
          15
S2.6
              S25 AND DEGENERAT?
              S25 AND REGENERAT?
S27
          66
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09/893,348

DIALUG

file bicsci
1/24/2003

	Type	Hits	Search Text	DBs
1	BRS	14	EISENBACH-SCHWARTZ-M	USPAT; US-PGPUB; EPO; JPO; DERWENT
2	BRS	16	EISENBACH-SCHWARTZ-MICHAL	USPAT; US-PGPUB; EPO; JPO; DERWENT
3	BRS	3	HAUBEN-EHUD	USPAT; US-PGPUB; EPO; JPO; DERWENT
4	BRS	55	COHEN-IRUN-R	USPAT; US-PGPUB; EPO; JPO; DERWENT
5	BRS	5	BESERMAN-PIERRE	USPAT; US-PGPUB; EPO; JPO; DERWENT
6	BRS	12	BESERMAN	USPAT; US-PGPUB; EPO; JPO; DERWENT
7	BRS	2	MOSONEGO-ALON	USPAT; US-PGPUB; EPO; JPO; DERWENT
8	BRS	2	MOALEM-GILA	USPAT; US-PGPUB; EPO; JPO; DERWENT
9	BRS	266	Nogo	USPAT; US-PGPUB; EPO; JPO; DERWENT
10	BRS	9	Nogo and neuro\$	USPAT; US-PGPUB; EPO; JPO; DERWENT
11	BRS	12	p472	USPAT; US-PGPUB; EPO; JPO; DERWENT
12	BRS	10	Nogo and central adj nervous adj system	USPAT; US-PGPUB; EPO; JPO; DERWENT
13	BRS	6	nogo and spinal adj cord	USPAT; US-PGPUB; EPO; JPO; DERWENT

c9/893,348

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